

Rooke 10/015, 956

=> d his

(FILE 'HOME' ENTERED AT 09:23:47 ON 02 AUG 2005)

FILE 'REGISTRY' ENTERED AT 09:23:53 ON 02 AUG 2005  
L1 26021 S EGEG/SQSP

FILE 'HCAPLUS' ENTERED AT 09:25:27 ON 02 AUG 2005  
L2 4892 S L1  
L3 643 S (FUSION OR CHIMER? OR CHIMAER?) (5A) PROTEIN? AND L2  
L4 6 S L3 AND CAPTUR?  
L5 0 S L3 AND POLYCATION?  
L6 2 S L2 AND POLYCATION?  
SELECT L6 RN 1-2  
L7 361075 S E1-828

FILE 'REGISTRY' ENTERED AT 09:32:39 ON 02 AUG 2005  
L8 0 S (AG){3-6}EG{14-36}/SQSP  
L9 271929 S (AG){0-8}EG{2-40}/SQSP  
L10 271887 S .{2-}(AG){0-8}EG{2-40}|(AG){0-8}EG{2-40}.{2-}/SQSP  
L11 271858 S SQL>=6 AND L10

FILE 'HCAPLUS' ENTERED AT 09:58:13 ON 02 AUG 2005  
L12 32705 S L11  
L13 10387 S L12 AND ?CATION?

FILE 'REGISTRY' ENTERED AT 10:01:10 ON 02 AUG 2005  
L14 26011 S .{2-}(AG){0-8}(EG){2-40}|(AG){0-8}(EG){2-40}.{2-}/SQSP  
L15 146 S .{2-}(AG){0-8}(PEG){2-40}|(AG){0-8}(PEG){2-40}.{2-}/SQSP  
L16 26156 S L14 OR L15

FILE 'HCAPLUS' ENTERED AT 10:06:00 ON 02 AUG 2005  
L17 4920 S L16  
L18 2014 S L17 AND ?CATION?  
L19 15 S L18 AND CAPTUR?  
L20 25 S L18 AND SOLID(3A) SUPPORT?  
L21 0 S L20 AND TAIL?  
L22 44 S L18 AND TAIL?  
L23 1 S L18 AND ?POLYMER?(3A) TAIL?  
L24 3 S L18 AND TETHER?  
L25 2011 S L18 NOT L24  
L26 2 S L25 AND POSITIV? AND NEGATIV?  
L27 2009 S L25 NOT L26  
L28 1 S L27 AND POLYLYSINE?  
L29 2 S L17 AND POLYLYSINE?

FILE 'REGISTRY' ENTERED AT 11:17:51 ON 02 AUG 2005  
L30 1 S 775512-26-0

FILE 'HCAPLUS' ENTERED AT 11:25:29 ON 02 AUG 2005

FILE 'REGISTRY' ENTERED AT 11:27:21 ON 02 AUG 2005  
L31 1 S 775512-27-1  
L32 26011 S .{2-}(AG){0-8}(EG){2-40}^|^^(AG){0-8}(EG){2-40}.{2-}|^.{2-}(AG  
L33 146 S .{2-}(AG){0-8}(PEG){2-40}^|^(AG){0-8}(PEG){2-40}.{2-}|^.{2-}(  
L34 26156 S L32 OR L33

FILE 'HCAPLUS' ENTERED AT 11:46:33 ON 02 AUG 2005  
L35 4920 S L34  
L36 1 S L27 AND POLYARGININE

Rooke 10/015,956

L37 1 S L17 AND POLYARGININE  
L38 1 S L17 AND POLYARGININE?  
L39 2 S L27 AND ANION?(2A)BIND?  
L40 4 S L27 AND CATION(2A)BIND?  
L41 2 S L27 AND ?ANION?(2A)(BIND? OR BOUND?)  
L42 51 S L27 AND ?CATION?(2A)BIND?  
L43 0 S L27 AND ?CATION?(2A)BOUND?  
L44 1 S L42 AND MATRI?  
L45 50 S L42 NOT L44  
L46 79 S L4 OR L6 OR L19 OR L24 OR L28 OR L29 OR L36-L45  
L47 13 S PY<2001 AND L46  
DELETE SELECT  
SELECT L47 RN 1-13  
DELETE SELECT

FILE 'REGISTRY' ENTERED AT 12:11:11 ON 02 AUG 2005

FILE 'HCAPLUS' ENTERED AT 12:11:23 ON 02 AUG 2005  
L48 TRA L47 1-13 RN : 4216 TERMS

FILE 'REGISTRY' ENTERED AT 12:11:25 ON 02 AUG 2005  
L49 4216 SEA L48  
L50 58 S L49 AND L16

FILE 'HCAPLUS' ENTERED AT 12:13:54 ON 02 AUG 2005  
L51 13 S L47 AND L50

=> d ibib abs 151 1-13

L51 ANSWER 1 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN  
ACCESSION NUMBER: 2003:42910 HCAPLUS  
DOCUMENT NUMBER: 138:102669  
TITLE: Engineered construction of long-wavelength variants of  
Aequorea green fluorescent protein by computational  
modeling from its three-dimensional crystal structure  
INVENTOR(S): Wachter, Rebekka M.; Remington, S. James  
PATENT ASSIGNEE(S): USA  
SOURCE: U.S. Pat. Appl. Publ., 100 pp., Cont.-in-part of U. S.  
6,077,707.  
CODEN: USXXCO  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 4  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003013149	A1	20030116	US 2000-575847	20000519
US 6593135	B2	20030715		
US 6124128	A	20000926	US 1996-706408	19960830 <--
US 6054321	A	20000425	US 1997-911825	19970815 <--
EP 1508574	A2	20050223	EP 2004-24850	19970815
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 6077707	A	20000620	US 1997-974737	19971119 <--
AU 767375	B2	20031106	AU 2001-23196	20010223
CA 2408302	AA	20011129	CA 2001-2408302	20010517
WO 2001090147	A2	20011129	WO 2001-US16149	20010517
WO 2001090147	A3	20020502		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,				

CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,  
 HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,  
 LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,  
 RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,  
 YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,  
 DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,  
 BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG  
 EP 1285065 A2 20030226 EP 2001-937550 20010517  
 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,  
 IE, SI, LT, LV, FI, RO, MK, CY, AL, TR  
 JP 2004502410 T2 20040129 JP 2001-586334 20010517  
 US 2004014128 A1 20040122 US 2003-620099 20030714  
 PRIORITY APPLN. INFO.:  
 US 1996-24050P P 19960816  
 US 1996-706408 A1 19960830  
 US 1997-911825 A1 19970815  
 US 1997-974737 A2 19971119  
 AU 1997-43277 A3 19970815  
 EP 1997-941350 A3 19970815  
 US 2000-575847 A 20000519  
 WO 2001-US16149 W .20010517

AB Engineered fluorescent proteins, nucleic acids encoding them, and methods of use are provided. As a step in understanding the properties of green fluorescent protein (GFP) from *Aequorea victoria*, and to aid in the tailoring of GFPs with altered characteristics, the 3-dimensional structure was determined at 1.9 Å resolution of the S65T mutant. Spectral properties of Thr203 mutants in comparison to S65T are provided. In particular, the S65G/V68L/S72A/T203Y (designated yellow fluorescent protein or YFP) displays an excitation maximum at 514 nm, an emission maximum

at 527 nm, extinction coefficient of 83,400 M-1cm-1, and quantum yield of 0.61; its absorption spectrum is a function of NaCl concentration, demonstrating its usefulness as a halide sensor. Crystallog. **identification** and description of halide binding sites indicates a relationship between **anion binding** and cavity size, a relaxation of the β-barrel conformation in response to the H148Q substitution and iodide binding, and the key residues for **anion binding** are determined by mutational anal.

L51 ANSWER 2 OF 13 HCPLUS COPYRIGHT 2005 ACS on STN  
 ACCESSION NUMBER: 2000:717215 HCPLUS  
 DOCUMENT NUMBER: 134:176440  
 TITLE: **Identification** of nucleolar protein No55 as a tumour-associated autoantigen in patients with prostate cancer  
 AUTHOR(S): Fossa, A.; Siebert, R.; Aasheim, H.-C.; Maelandsmo, G. M.; Berner, A.; Fossa, S. D.; Paus, E.; Smeland, E. B.; Gaudernack, G.  
 CORPORATE SOURCE: Department of Immunology, The Norwegian Radium Hospital, Oslo, 0310, Norway  
 SOURCE: British Journal of Cancer (2000), 83(6), 743-749  
 CODEN: BJCAAI; ISSN: 0007-0920  
 PUBLISHER: Harcourt Publishers Ltd.  
 DOCUMENT TYPE: Journal  
 LANGUAGE: English  
 AB Four different genes were identified by immunoscreening of a cDNA expression library from the human prostate cancer cell line DU145 with allogeneic sera from four prostate cancer patients. A cDNA encoding the nucleolar protein No55 was further analyzed and shown to be expressed at

the mRNA level in several normal tissues, including ovaries, pancreas and prostate and in human prostate cancer cell lines PC-3, PC-3m and LNCaP. By reverse transcriptase/polymerase chain reaction, expression of No55 was several-fold higher in two out of nine prostate cancer primary tumors and two out of two metastatic lesions, compared to normal prostate tissue. Antibodies to No55 were detected in sera from seven out of 47 prostate cancer patients but not in sera from 20 healthy male controls. Sequence anal. of the No55 open reading frame from normal and tumor tissues revealed no tumor-specific mutations. The No55 gene was located to chromosome 17q21, a region reported to be partially deleted in prostate cancer. Considering the immunogenicity of the No55 protein in the tumor host, the expression profile and chromosomal localization of the corresponding gene, studies evaluating No55 as a potential antigen for immunol. studies in prostate cancer may be warranted.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 3 OF 13 HCPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:697875 HCPLUS

DOCUMENT NUMBER: 134:290979

TITLE: Isoforms of JSAP1 scaffold protein generated through alternative splicing

AUTHOR(S): Ito, M.; Akechi, M.; Hirose, R.; Ichimura, M.; Takamatsu, N.; Xu, P.; Nakabeppu, Y.; Tadayoshi, S.; Yamamoto, K.-i.; Yoshioka, K.

CORPORATE SOURCE: School of Science, Department of Biosciences, Kitasato University, Sagamihara, Kanagawa, 228-8555, Japan

SOURCE: Gene (2000), 255(2), 229-234  
CODEN: GENED6; ISSN: 0378-1119

PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We have identified four isoforms of c-Jun NH<sub>2</sub>-terminal kinase (JNK)/stress-activated protein kinase-associated protein 1 (JSAP1), a scaffold protein that participates in JNK mitogen-activated protein kinase cascades, termed JSAP1a, JSAP1b, JSAP1c, and JSAP1d. The previously identified JSAP1 was renamed JSAP1a to avoid confusion. Analyses of the exon-intron structure of the jsap1 gene indicated that the isoforms are generated through alternative splicing involving exons 5 and 6. The mRNA expression levels of the JSAP1 isoforms differed among the mouse tissues examined. We also investigated the region of JSAP1 responsible for its interaction with JNK, and found that the JNK-binding domain is located between aa residues 201 and 217 in JSAP1a, which is encoded by part of exon 6. As all the JSAP1 isoforms contain this binding domain, we examined the binding affinity of the JSAP1 isoforms for JNK1, JNK2, and JNK3. JSAP1c and JSAP1d, which contain a 31-aa sequence not present in JSAP1a or JSAP1b, had a lower binding affinity for the JNKs, especially JNK3. These results suggest that JSAP1c and JSAP1d may attenuate the scaffolding activity of JSAP1a and/or JSAP1b in JNK cascades, especially the JNK3 cascades.

REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 4 OF 13 HCPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:627482 HCPLUS

DOCUMENT NUMBER: 133:262900

TITLE: Sequence similarities between a novel putative G protein-coupled receptor and Na<sup>+</sup>/Ca<sup>2+</sup> exchangers define a cation binding domain

AUTHOR(S): Nikkila, Heli; McMillan, D. Randy; Nunez, Brian S.; Pascoe, Leigh; Curnow, Kathleen M.; White, Perrin C.

CORPORATE SOURCE: Division of Pediatric Endocrinology, University of Texas Southwestern Medical Center, Dallas, TX, 75235-9063, USA

SOURCE: Molecular Endocrinology (2000), 14(9), 1351-1364

CODEN: MOENEN; ISSN: 0888-8809

PUBLISHER: Endocrine Society

DOCUMENT TYPE: Journal

LANGUAGE: English

AB CDNA clones encoding a novel putative G protein-coupled receptor have been characterized. The receptor is widely expressed in normal solid tissues. Consisting of 1967 amino acid residues, this receptor is one of the largest known and is therefore referred to as a very large G protein-coupled receptor, or VLGR1. It is most closely related to the secretin family of G protein-coupled receptors based on similarity of the sequences of its transmembrane segments. As demonstrated by cell surface labeling with a biotin derivative, the recombinant protein is expressed on the surface of transfected mammalian cells. Whereas several other recently described receptors in this family also have large extracellular domains, the large extracellular domain of VLGR1 has a unique structure. It has nine imperfectly repeated units that are rich in acidic residues and are spaced at intervals of approx. 120 amino acid residues. These repeats resemble the regulatory domains of Na<sup>+</sup>/Ca<sup>2+</sup> exchangers as well as a component of an extracellular aggregation factor of marine sponges. Bacterial fusion proteins containing two or four repeats specifically bind 45Ca in overlay expts.; binding is competed poorly by Mg<sup>2+</sup> but competed well by neomycin, Al<sup>3+</sup>, and Gd<sup>3+</sup>. These results define a consensus cation binding motif employed in several widely divergent types of proteins. The ligand for VLGR1, its function, and the signaling pathway(s) it employs remain to be defined.

REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 5 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:613167 HCAPLUS

DOCUMENT NUMBER: 133:218310

TITLE: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae

AUTHOR(S): Heidelberg, John F.; Elsen, Jonathan A.; Nelson, William C.; Clayton, Rebecca A.; Gwinn, Michelle L.; Dodson, Robert J.; Haft, Daniel H.; Hickey, Erin K.; Peterson, Jeremy D.; Umayam, Lowell; Gill, Steven R.; Nelson, Karen E.; Read, Timothy D.; Tettelin, Herve; Richardson, Delwood; Ermolaeva, Maria D.; Vamathevan, Jessica; Bass, Steven; Qin, Haiying; Dragoi, Loana; Sellers, Patrick; McDonald, Lisa; Utterback, Teresa; Fleishmann, Robert D.; Nierman, William C.; White, Owen; Salzberg, Steven L.; Smith, Hamilton O.; Colwell, Rita R.; Mekalanos, John J.; Venter, J. Craig; Fraser, Claire M.

CORPORATE SOURCE: The Institute for Genomic Research, Rockville, MD, 20850, USA

SOURCE: Nature (London) (2000), 406(6795), 477-483

CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The complete genomic sequence of the gram-neg.,  $\gamma$ -Proteobacterium Vibrio cholerae El Tor N16961 was determined to be 4,033,460 bp. The genome consists of two circular chromosomes of 2,961,146 bp and 1,072,314 bp that

together encode 3885 open reading frames. The vast majority of recognizable genes for essential cell functions (such as DNA replication, transcription, translation, and cell-wall biosynthesis) and pathogenicity (for example, toxins, surface antigens, and adhesins) are located on the large chromosome. In contrast, the small chromosome contains a larger fraction (59%) of hypothetical genes compared with the large chromosome (42%), and also contains many more genes that appear to have origins other than the  $\gamma$ -Proteobacteria. The small chromosome also carries a gene capture system (the integron island) and host 'addiction' genes that are typically found on plasmids; thus, the small chromosome may have originally been a megaplasmid that was captured by an ancestral Vibrio species. The V. cholerae genomic sequence provides a starting point for understanding how a free-living, environmental organism emerged to become a significant human bacterial pathogen.

REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 6 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:4884 HCAPLUS

DOCUMENT NUMBER: 132:163331

TITLE: env sequences of simian immunodeficiency viruses from chimpanzees in Cameroon are strongly related to those of human immunodeficiency virus group N from the same geographic area

AUTHOR(S): Corbet, Sylvie; Muller-Trutwin, Michaela C.; Versmisse, Pierre; Delarue, Severine; Ayouba, Ahidjo; Lewis, John; Brunak, Soren; Martin, Paul; Brun-Vezinet, Francoise; Simon, Francois; Barre-Sinoussi, Francoise; Mauclere, Philippe

CORPORATE SOURCE: Unite de Biologie des Retrovirus, Institut Pasteur, Paris, Fr.

SOURCE: Journal of Virology (2000), 74(1), 529-534

CODEN: JOVIAM; ISSN: 0022-538X

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Human immunodeficiency virus type 1 (HIV-1) group N from Cameroon is phylogenetically close, in env, to the simian immunodeficiency virus (SIV) cpz-gab from Gabon and SIVcpz-US of unknown geog. origin. We screened 29 wild-born Cameroonian chimpanzees and found that three (Cam3, Cam4, and Cam5) were pos. for HIV-1 by Western blotting. Mitochondrial DNA sequence anal. demonstrated that Cam3 and Cam5 belonged to Pan troglodytes troglodytes and that Cam4 belonged to P. t. vellerosus. Genetic analyses of the viruses together with serol. data demonstrated that at least one of the two P. t. troglodytes chimpanzees (Cam5) was infected in the wild, and revealed a horizontal transmission between Cam3 and Cam4. These data confirm that P. t. troglodytes is a natural host for HIV-1-related viruses. Furthermore, they show that SIVcpz can be transmitted in captivity, from one chimpanzee subspecies to another. All three SIVcpz-cam viruses clustered with HIV-1 N in env. The full Cam3 SIVcpz genome sequence showed a very close phylogenetic relationship with SIVcpz-US, a virus identified in a P. t. troglodytes chimpanzee captured nearly 40 yr earlier. Like SIVcpz-US, SIVcpz-cam3 was closely related to HIV-1 N in env, but not in pol, supporting the hypothesis that HIV-1 N results from a recombination event. SIVcpz from chimpanzees born in the wild in Cameroon are thus strongly related in env to HIV-1 N from Cameroon, demonstrating the geog. coincidence of these human and simian viruses and providing a further strong argument in favor of the origin of HIV-1 being in chimpanzees.

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 7 OF 13 HCPLUS COPYRIGHT 2005 ACS on STN  
 ACCESSION NUMBER: 1999:766689 HCPLUS  
 DOCUMENT NUMBER: 132:133025  
 TITLE: Identification of a Novel Homolog of the Drosophila staufen Protein in the Chromosome 8q13-q21.1 Region  
 AUTHOR(S): Buchner, Georg; Bassi, Maria Teresa; Andolfi, Grazia; Ballabio, Andrea; Franco, Brunella  
 CORPORATE SOURCE: Telethon Institute of Genetics and Medicine (TIGEM), Milan, Italy  
 SOURCE: Genomics (1999), 62(1), 113-118  
 CODEN: GNMCEP; ISSN: 0888-7543  
 PUBLISHER: Academic Press  
 DOCUMENT TYPE: Journal  
 LANGUAGE: English

AB We report the identification of a new transcript homologous to the Drosophila staufen protein. This transcript, named STAU2 (HGMW-approved gene symbol and name), maps to the chromosome 8q13-q21 region. The full-length STAU2 cDNA is 4058 bp and contains an open reading frame of 479 amino acids. Anal. of the predicted protein product indicated the presence of three double-stranded RNA-binding domains. Best-fit anal. revealed a 48.5% similarity to the Drosophila protein and a 59.9% similarity to the recently described mammalian homolog hStau, indicating that at least two different transcripts with homologies to the fly protein are present in mammals. (c) 1999 Academic Press.

REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 8 OF 13 HCPLUS COPYRIGHT 2005 ACS on STN  
 ACCESSION NUMBER: 1999:594265 HCPLUS  
 DOCUMENT NUMBER: 131:320676  
 TITLE: mAKAP: an A-kinase anchoring protein targeted to the nuclear membrane of differentiated myocytes  
 AUTHOR(S): Kapiloff, Michael S.; Schillace, Robynn V.; Westphal, Ann M.; Scott, John D.  
 CORPORATE SOURCE: Howard Hughes Medical Institute, Vollum Institute, Portland, OR, 97201-3098, USA  
 SOURCE: Journal of Cell Science (1999), 112(16), 2725-2736  
 CODEN: JNCBAI; ISSN: 0021-9533  
 PUBLISHER: Company of Biologists Ltd.  
 DOCUMENT TYPE: Journal  
 LANGUAGE: English  
 AB The compartmentalization of second messenger-activated protein kinases contributes to the fidelity of hormone-mediated signal transduction events. For example, the cAMP-dependent protein kinase is tethered at specific intracellular locations through association with A-kinase anchoring proteins (AKAPs). The authors now report the cloning of mAKAP, an anchoring protein found predominantly in heart, skeletal muscle and brain, and whose expression is induced in neonatal ventriculocytes by treatment with hypertrophic stimuli. MAKAP is targeted to the nuclear membrane of differentiated myocytes. Anal. of mAKAP-green fluorescent protein (GFP) fusion constructs revealed that nuclear membrane targeting is conferred by two regions of the protein, between residues 772-915 and 915-1065, which contain spectrin-like repeat sequences. Heterologous expression of the mAKAP targeting sequences displaced the endogenous anchoring protein from the nuclear membrane, demonstrating that

mAKAP targeting is saturable. Collectively, these data suggest that a domain containing spectrin-like repeats mediates targeting of the anchoring protein mAKAP and the cAMP-dependent protein kinase holoenzyme to the nuclear membrane in response to differentiation signals.

REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 9 OF 13 HCPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1998:460763 HCPLUS

DOCUMENT NUMBER: 129:185689

TITLE: Identification of a human PTS1 receptor docking protein directly required for peroxisomal protein import

AUTHOR(S): Fransen, Marc; Terlecky, Stanley R.; Subramani, Suresh

CORPORATE SOURCE: Department of Biology, University of California at San Diego, La Jolla, CA, 92093-0322, USA

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1998), 95(14), 8087-8092

CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The discovery of many fatal human disorders resulting from impaired peroxisomal protein import makes the functional characterization of human peroxins critical. As part of our attempt to identify novel human genes and gene products involved in the import of peroxisomal proteins, the authors raised antisera against peroxisomal membrane proteins. One such antiserum inhibited peroxisomal protein import in semipermeabilized mammalian cells. This "import inhibiting" antiserum, ab-MF3, specifically recognized a 57-kDa protein. Immunoblot anal. of rat liver subcellular fractions demonstrated that this protein was present exclusively in peroxisomal membranes. Functional anal. revealed that this 57-kDa mol. bound the PTS1 receptor, Tcx5p, in ligand blots, suggesting it is a docking site on the peroxisomal membrane. Previous studies have identified two yeast proteins, Pex14p and Pex13p, as Pex5p-binding proteins. To facilitate the biochem. anal. of peroxisomal membrane docking proteins, the authors cloned and expressed the previously unidentified human Pex14p, as well as a human Pex13p that is 39 aa longer than previously reported. Recombinant Pex14p was specifically recognized by the "import inhibiting" ab-MF3 and bound Pex5p and the Src homol. 3 (SH3) domain of Pex13p in ligand blots. These studies demonstrate that the ab-MF3-immunoreactive, 57-kDa peroxisomal membrane protein is Pex14p. Furthermore, this peroxin interacts with Pex5p and Pex13p(SH3) and is directly required for peroxisomal protein import.

REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 10 OF 13 HCPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1996:424017 HCPLUS

DOCUMENT NUMBER: 125:110877

TITLE: Association of human protein-tyrosine phosphatase κ with members of the Armadillo family

AUTHOR(S): Fuchs, Miriam; Mueller, Thomas; Lerch, Markus M.; Ullrich, Axel

CORPORATE SOURCE: Dep. Molecular Biol., Max-Planck-Inst. Biochemie, Martinsried, 82152, Germany

SOURCE: Journal of Biological Chemistry (1996), 271(28), 16712-16719

CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular

Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A human receptor-like protein-tyrosine phosphatase (PTP) was identified in the mammary carcinoma cell line SK-BR-3, which represents the human homolog of murine PTP $\kappa$  and was therefore termed hPTP $\kappa$ . The hPTP $\kappa$  expression is dependent on cell d. and is colocalized with 2 members of the arm family of proteins,  $\beta$ -catenin and  $\gamma$ -catenin/plakoglobin, at adherens junctions. Both in vitro and in vivo binding assays demonstrated specific complex formation between endogenous hPTP $\kappa$  and  $\beta$ - and  $\gamma$ -catenin/plakoglobin. In addition, evidence that suggests that  $\beta$ -catenin may represent a substrate for the catalytic activity of hPTP $\kappa$ . The identification of specific binding partners for this receptor-like PTP provides insight into the mechanisms of its biol. action and suggests a role for hPTP $\kappa$  in the regulation of processes involving cell contact and adhesion such as growth control, tumor invasion, and metastasis.

L51 ANSWER 11 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1996:137493 HCAPLUS

DOCUMENT NUMBER: 124:222269

TITLE: Identification and characterization of a thermostable MutS homolog from *Thermus aquaticus*

AUTHOR(S): Biswas, Indranil; Hsieh, Peggy

CORPORATE SOURCE: Genetics & Biochemistry Branch, NIDDK, Bethesda, MD, 20892-1810, USA

SOURCE: Journal of Biological Chemistry (1996), 271(9), 5040-8

CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Recognition of mispaired or unpaired bases during DNA mismatch repair is carried out by the MutS protein family. Here, the authors describe the isolation and characterization of a thermostable MutS homolog from *Thermus aquaticus* YT-1. Sequencing of the mutS gene predicts an 89.3-kDa polypeptide sharing extensive amino acid sequence homol. with MutS homologs from both prokaryotes and eukaryotes. Expression of the *T. aquaticus* mutS gene in *Escherichia coli* results in a dominant mutator phenotype. Initial biochem. characterization of the thermostable MutS protein, which was purified to apparent homogeneity, reveals two thermostable activities, an ATP hydrolysis activity in which ATP is hydrolyzed to ADP and Pi and a specific DNA mismatch binding activity with affinities for heteroduplex DNAs containing either an insertion/deletion of one base or a GT mismatch. The ATPase activity exhibits a temperature optimum of approx. 80°C. Heteroduplex DNA binding by the *T. aquaticus* MutS protein requires Mg<sup>2+</sup> and occurs over a broad temperature range from 0°C to at least 70°C. The thermostable MutS protein may be useful for further biochem. and structural studies of mismatch binding and for applications involving mutation detection.

L51 ANSWER 12 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1995:301696 HCAPLUS

DOCUMENT NUMBER: 122:179969

TITLE: Nucleotide sequence and mutational analysis indicate that two *Helicobacter pylori* genes encode a P-type ATPase and a cation-binding

AUTHOR(S): protein associated with copper transport  
CORPORATE SOURCE: Ge, Zhongming; Hiratsuka, Koji; Taylor, Diane E.  
Dep. Med. Microbiol. Infectious Diseases, Univ.  
Alberta, Edmonton, AB, T6G 2H7, Can.  
SOURCE: Molecular Microbiology (1995), 15(1), 97-106  
CODEN: MOMIEE; ISSN: 0950-382X  
PUBLISHER: Blackwell  
DOCUMENT TYPE: Journal  
LANGUAGE: English  
AB A 2.7-kb fragment of *Helicobacter pylori* UA802 chromosomal DNA was cloned and sequenced. Three open reading frames (designated ORF1, ORF2 and ORF3, resp.) were predicted from the DNA sequence, of which ORF1 and ORF2 appeared to be located within the same operon. The deduced 611-amino-acid sequence of ORF1, a P-type ATPase (designated hpCopA), had striking homol. (29-38%) with several bacterial P-type ATPases and contained the potential functional domains conserved in P-type ATPases from various sources ranging from bacterial to human. A protein of 66 amino acids (designated hpCopP) encoded by ORF2 shared extensive sequence similarity with MerP, a periplasmic mercuric ion-transporting protein, and contains the heavy metal-binding motif. Disruption of ORF1 with a chloramphenicol-resistance cassette (CAT) rendered the *H. pylori* mutants more susceptible to cupric ion than their parental strains, whereas there is no significant alteration of susceptibility to Ni<sup>2+</sup>, Cd<sup>2+</sup> and Hg<sup>2+</sup> between the mutants and the parental strains. The results obtained indicate that ORF1 and ORF2 comprise a cation-transporting system which is associated with copper export out of the *H. pylori* cells.

L51 ANSWER 13 OF 13 HCPLUS COPYRIGHT 2005 ACS on STN  
ACCESSION NUMBER: 1993:443606 HCPLUS  
DOCUMENT NUMBER: 119:43606  
TITLE: Identification and preliminary characterization of a protein motif related to the zinc finger  
AUTHOR(S): Lovering, Ruth; Hanson, Isabel M.; Borden, Katherine L. B.; Martin, Stephen; O'Reilly, Nicola J.; Evan, Gerard I.; Rahman, Dinah; Pappin, Darryl J. C.; Trowsdale, John; Freemont, Paul S.  
CORPORATE SOURCE: Hum. Immunogenet. Lab., Imp. Cancer Res. Fund, London, WC2A 3PX, UK  
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1993), 90(6), 2112-16  
CODEN: PNASA6; ISSN: 0027-8424  
DOCUMENT TYPE: Journal  
LANGUAGE: English  
AB A protein motif related to the zinc finger was identified which defines a newly discovered family of proteins. The motif was found in the sequence of the human RING1 gene, which is proximal to the major histocompatibility complex region on chromosome 6. The name RING finger is proposed for this motif, which is found in 27 proteins, all of which have putative DNA binding functions. A peptide corresponding to the RING1 motif was synthesized and a number of its properties, including metal and DNA binding, were examined. The RING finger motif appears to be the DNA-binding domain of this newly defined family of proteins.

=> d his full

(FILE 'HOME' ENTERED AT 09:23:47 ON 02 AUG 2005)

Rooke 10/015, 956

FILE 'REGISTRY' ENTERED AT 09:23:53 ON 02 AUG 2005  
L1 26021 SEA EGEG/SQSP

FILE 'HCAPLUS' ENTERED AT 09:25:27 ON 02 AUG 2005  
L2 4892 SEA L1  
L3 643 SEA (FUSION OR CHIMER? OR CHIMAER?) (5A) PROTEIN? AND L2  
L4 6 SEA L3 AND CAPTUR?  
L5 0 SEA L3 AND POLYCATION?  
L6 2 SEA L2 AND POLYCATION?  
D SCAN  
SELECT L6 RN 1-2

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L9 271929 SEA (AG){0-8}EG{2-40}/SQSP  
L10 271887 SEA .{2-} (AG){0-8}EG{2-40}|(AG){0-8}EG{2-40}.{2-}/SQSP  
L11 271858 SEA SQL>=6 AND L10

FILE 'HCAPLUS' ENTERED AT 09:58:13 ON 02 AUG 2005  
L12 32705 SEA L11  
L13 10387 SEA L12 AND ?CATION?

FILE 'REGISTRY' ENTERED AT 10:01:10 ON 02 AUG 2005  
L14 26011 SEA .{2-} (AG){0-8}(EG){2-40}|(AG){0-8}(EG){2-40}.{2-}/SQSP  
L15 146 SEA .{2-} (AG){0-8}(PEG){2-40}|(AG){0-8}(PEG){2-40}.{2-}/SQSP  
L16 26156 SEA L14 OR L15

Rooke 10/015, 956

FILE 'HCAPLUS' ENTERED AT 10:06:00 ON 02 AUG 2005

L17 4920 SEA L16  
L18 2014 SEA L17 AND ?CATION?  
L19 15 SEA L18 AND CAPTUR?  
L20 25 SEA L18 AND SOLID(3A) SUPPORT?  
L21 0 SEA L20 AND TAIL?  
L22 44 SEA L18 AND TAIL?  
L23 1 SEA L18 AND ?POLYMER?(3A) TAIL?  
D SCAN  
L24 3 SEA L18 AND TETHER?  
D SCAN  
L25 2011 SEA L18 NOT L24  
L26 2 SEA L25 AND POSITIV? AND NEGATIV?  
D SCAN  
L\*\*\* DEL 0 S L25 NOT L25  
L27 2009 SEA L25 NOT L26  
L\*\*\* DEL 0 S BLOCK(A) HOMOPOLYMER? (5A) AMINO (3A) ACID  
L\*\*\* DEL 18 S BLOCK(A) POLYMER? (5A) AMINO (3A) ACID  
D L27 TI 1-20  
L28 1 SEA L27 AND POLYLYSINE?  
D SCAN  
L29 2 SEA L17 AND POLYLYSINE?

FILE 'REGISTRY' ENTERED AT 11:17:51 ON 02 AUG 2005

L30 1 SEA 775512-26-0  
D SCAN  
D SQIDE L30

FILE 'HCAPLUS' ENTERED AT 11:25:29 ON 02 AUG 2005

D SCAN L29

FILE 'REGISTRY' ENTERED AT 11:27:21 ON 02 AUG 2005

L31 1 SEA 775512-27-1  
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L34 26156 SEA L32 OR L33

FILE 'HCAPLUS' ENTERED AT 11:46:33 ON 02 AUG 2005

L35 4920 SEA L34  
L36 1 SEA L27 AND POLYARGININE  
L37 1 SEA L17 AND POLYARGININE  
L38 1 SEA L17 AND POLYARGININE?  
L\*\*\* DEL 624 S L27 AND BIND?  
L39 2 SEA L27 AND ANION?(2A) BIND?  
L40 4 SEA L27 AND CATION(2A) BIND?  
D SCAN L39  
D SCAN  
L\*\*\* DEL 0 S L27 AND POLYANION?(2A) BIND?  
L41 2 SEA L27 AND ?ANION?(2A) (BIND? OR BOUND?)  
D SCAN  
L42 51 SEA L27 AND ?CATION?(2A) BIND?  
L43 0 SEA L27 AND ?CATION?(2A) BOUND?  
L44 1 SEA L42 AND MATRI?  
D SCAN  
L45 50 SEA L42 NOT L44  
D TI 1-2  
D TI 2-20

Rooke 10/015,956

L46 79 SEA L4 OR L6 OR L19 OR L24 OR L28 OR L29 OR (L36 OR L37 OR  
L38 OR L39 OR L40 OR L41 OR L42 OR L43 OR L44 OR L45)  
L47 13 SEA PY<2001 AND L46  
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SELECT L47 RN 1-13  
DELETE SELECT

FILE 'REGISTRY' ENTERED AT 12:11:11 ON 02 AUG 2005

FILE 'HCAPLUS' ENTERED AT 12:11:23 ON 02 AUG 2005  
L48 TRA L47 1-13 RN : 4216 TERMS

FILE 'REGISTRY' ENTERED AT 12:11:25 ON 02 AUG 2005  
L49 4216 SEA L48  
L50 58 SEA L49 AND L16  
L\*\*\* DEL 0 S HCAPLUS

FILE 'HCAPLUS' ENTERED AT 12:13:54 ON 02 AUG 2005  
L51 13 SEA L47 AND L50  
D IBIB ABS L51 1-13

FILE HOME

FILE REGISTRY

Property values tagged with IC are from the ZIC/VINITI data file  
provided by InfoChem.

STRUCTURE FILE UPDATES: 1 AUG 2005 HIGHEST RN 857935-17-2  
DICTIONARY FILE UPDATES: 1 AUG 2005 HIGHEST RN 857935-17-2

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TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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conducting SmartSELECT searches.

\*\*\*\*\*  
\*  
\* The CA roles and document type information have been removed from \*  
\* the IDE default display format and the ED field has been added, \*  
\* effective March 20, 2005. A new display format, IDERL, is now \*  
\* available and contains the CA role and document type information. \*  
\*  
\*\*\*\*\*

Structure search iteration limits have been increased. See HELP SLIMITS  
for details.

Experimental and calculated property data are now available. For more  
information enter HELP PROP at an arrow prompt in the file or refer  
to the file summary sheet on the web at:  
<http://www.cas.org/ONLINE/DBSS/registryss.html>

FILE HCAPLUS

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PASSWORD:

\* \* \* \* \* RECONNECTED TO STN INTERNATIONAL \* \* \* \* \*

=> d his

(FILE 'HOME' ENTERED AT 09:23:47 ON 02 AUG 2005)

L1 FILE 'REGISTRY' ENTERED AT 09:23:53 ON 02 AUG 2005  
26021 S EGEG/SQSP

L2 FILE 'HCAPLUS' ENTERED AT 09:25:27 ON 02 AUG 2005  
4892 S L1  
L3 643 S (FUSION OR CHIMER? OR CHIMAER?) (5A) PROTEIN? AND L2  
L4 6 S L3 AND CAPTUR?  
L5 0 S L3 AND POLYCATION?  
L6 2 S L2 AND POLYCATION?  
SELECT L6 RN 1-2  
L7 361075 S E1-828

L8 FILE 'REGISTRY' ENTERED AT 09:32:39 ON 02 AUG 2005  
0 S (AG){3-6}EG{14-36}/SQSP  
L9 271929 S (AG){0-8}EG{2-40}/SQSP  
L10 271887 S .{2-}(AG){0-8}EG{2-40}|(AG){0-8}EG{2-40}.{2-}/SQSP  
L11 271858 S SQL>=6 AND L10

L12 FILE 'HCAPLUS' ENTERED AT 09:58:13 ON 02 AUG 2005  
32705 S L11  
L13 10387 S L12 AND ?CATION?

L14 FILE 'REGISTRY' ENTERED AT 10:01:10 ON 02 AUG 2005  
26011 S .{2-}(AG){0-8}(EG){2-40}|(AG){0-8}(EG){2-40}.{2-}/SQSP  
L15 146 S .{2-}(AG){0-8}(PEG){2-40}|(AG){0-8}(PEG){2-40}.{2-}/SQSP  
L16 26156 S L14 OR L15

L17 FILE 'HCAPLUS' ENTERED AT 10:06:00 ON 02 AUG 2005  
4920 S L16  
L18 2014 S L17 AND ?CATION?  
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L20 25 S L18 AND SOLID(3A) SUPPORT?  
L21 0 S L20 AND TAIL?  
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L24 3 S L18 AND TETHER?  
L25 2011 S L18 NOT L24  
L26 2 S L25 AND POSITIV? AND NEGATIV?  
L27 2009 S L25 NOT L26  
L28 1 S L27 AND POLYLYSINE?  
L29 2 S L17 AND POLYLYSINE?

FILE 'REGISTRY' ENTERED AT 11:17:51 ON 02 AUG 2005

L30 1 S 775512-26-0  
FILE 'HCAPLUS' ENTERED AT 11:25:29 ON 02 AUG 2005  
FILE 'REGISTRY' ENTERED AT 11:27:21 ON 02 AUG 2005  
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FILE 'HCAPLUS' ENTERED AT 11:46:33 ON 02 AUG 2005  
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L37 1 S L17 AND POLYARGININE  
L38 1 S L17 AND POLYARGININE?  
L39 2 S L27 AND ANION?(2A)BIND?  
L40 4 S L27 AND CATION(2A)BIND?  
L41 2 S L27 AND ?ANION?(2A)(BIND? OR BOUND?)  
L42 51 S L27 AND ?CATION?(2A)BIND?  
L43 0 S L27 AND ?CATION?(2A)BOUND?  
L44 1 S L42 AND MATRI?  
L45 50 S L42 NOT L44  
L46 79 S L4 OR L6 OR L19 OR L24 OR L28 OR L29 OR L36-L45  
L47 13 S PY<2001 AND L46  
DELETE SELECT  
SELECT L47 RN 1-13  
DELETE SELECT  
FILE 'REGISTRY' ENTERED AT 12:11:11 ON 02 AUG 2005  
FILE 'HCAPLUS' ENTERED AT 12:11:23 ON 02 AUG 2005  
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FILE 'HCAPLUS' ENTERED AT 12:13:54 ON 02 AUG 2005  
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L52 846 S L17 AND (FUSION OR CHIMER? OR CHIMAER?)  
L53 302 S L52 AND BIND?  
L54 27 S L53 AND (IMMOBILIZ? OR IMMOBILIS?)  
L55 3 S L54 AND PY<2001  
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L56 69 S E1-E69  
L57 3 S L56 AND L16  
=> fil hcaplus  
FILE 'HCAPLUS' ENTERED AT 12:56:27 ON 02 AUG 2005  
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FILE COVERS 1907 - 2 Aug 2005 VOL 143 ISS 6  
FILE LAST UPDATED: 1 Aug 2005 (20050801/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s 157  
L58 . 4 L57

=> s 157 and 155  
L59 . 4 L57  
3 L57 AND L55

=> d sqide 157 1-3

L57 ANSWER 1 OF 3 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 283617-63-0 REGISTRY  
CN Peptide (synthetic) fusion protein with green fluorescent protein (Aequorea victoria) fusion protein with peptide (synthetic linker) fusion protein with anti-(human chorionic gonadotropin  $\alpha$ -subunit) immunoglobulin (Lama glama heavy chain V-D-J region) fusion protein with anti-(red reactive 6) immunoglobulin (Lama glama heavy chain V-D-J region) fusion protein with peptide (synthetic myc tag) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 44: PN: WO0040968 SEQID: 43 claimed protein  
FS PROTEIN SEQUENCE  
SQL 500

PATENT ANNOTATIONS (PNTE):

Sequence | Patent

Source | Reference

=====+=====

Not Given | WO2000040968

| claimed

| SEQID 43

SEQ 1 HHHHHHGSYG IHRPVATMVS KGEELFTGVV PILVELDGDV NGHKFSVSQE  
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51 GEGDATYGKL TLKFICTTGK LPVPWPTLVT TLTYGVQCFS RYPDHMKQHD  
=====+=====+=====+=====+=====+=====+=====+=====+=====+  
101 FFKSAMPEGY VQERTIFFKD DGNYKTRAEV KFEGDTLVNR IELKGIDFKE  
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151 DGNILGHKLE YNYNSHNVYI MADKQKNGIK VNFKIRHNIE DGSVQLADHY  
=====+=====+=====+=====+=====+=====+=====+=====+=====+  
201 QQNTPIGDGP VLLPDNHYLS TQSALSKDPN EKRDHMVLLE FVTAAGITGG  
=====+=====+=====+=====+=====+=====+=====+=====+=====+  
251 SGGGGSSQVK LLESGGELVQ PGGSLKLSCA ASGLTFTNYS MGWFRPGPGV  
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301 DREAVAAISW SGDNTYYVSS VKGRFTISRD NAKNTVYLQM NSLKPQDTAV

' 351 YYCAVKPDDG WWDYWGQGTQ VTVSSQVQLQ ESGGGLVQAG ESLKLSCAAS  
===== 401 GNTFSGGFMG WYRQAPGKQR ELVATINSRG ITNYADFVKG RFTISRDNAK  
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HITS AT: 1-500

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

DT.CA Cplus document type: Patent

RL.P Roles from patents: BIOL (Biological study); PRP (Properties); USES  
(Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L57 ANSWER 2 OF 3 REGISTRY COPYRIGHT 2005 ACS on STN

RN 158935-45-6 REGISTRY

CN 5-13-Dynorphin B [5-methionine,6-alanine] (synthetic clone pLM138) fusion  
protein with protein (synthetic 84-amino acid fragment) (9CI) (CA INDEX  
NAME)

FS PROTEIN SEQUENCE

SQL 93

SEQ 1 MARQFKVVTE FSGSGSGSGS GSGSGSGSGS GSGSGSGSGG SSAAVPAAVP  
===== 51 AAVPAAVPAA VPAAVPAAVS TEEGEGEGEKG EGRQATRRQQ APS  
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HITS AT: 1-93

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Cplus document type: Journal

RL.NP Roles from non-patents: PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L57 ANSWER 3 OF 3 REGISTRY COPYRIGHT 2005 ACS on STN

RN 138361-59-8 REGISTRY

CN Laminin (human clone 129/123/7 A-subunit precursor protein moiety reduced)  
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN Laminin (human A-subunit precursor)

FS PROTEIN SEQUENCE

SQL 3075

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===== 51 KLVEHVPGRP VRNPQCRCID GNSANPRERH PISHAIDGTN NWWQSPSIQN  
===== 101 GREYHWVTIT LDLRQVFQVA YVIKAANAP RPGNWILERS LDGTTFSPWQ  
===== 151 YYAVSDSECL SRYNITPRRG PPTYRADDEV ICTSYYSRLV PLEHGEIHTS  
===== 201 LINGRPSADD LSPKLLEFTS ARYIRLRLQR IRTLNADLMT LSHREPKELD  
===== 251 PIVTRRYYYS IKDISVGGM C ICYGHASSCP WDETTKKLQC QCEHNTCGES

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351 TAGQFRGGGV CINCLQNTMG INCETCIDGY YRPHKVSPYE DEPCRPCNCD
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401 PVGSLSSVCI KDDLHSDLHN GKQPGQCPCPK EGYTGEKCDR CQLGYKDYPY
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451 CVSCGCPVG SASDEPCTGP CVCKENVEGK ACDRCKPGFY NLKEKNPRGC
=====
501 SECFCFGVSD VCSSLSPVVG QVNMSGWLV TDLISPRKIP SQQDALGGRH
=====
551 QVSINNTAVM QRLAPKYYWA APEAYLGNKL TAFGGFLKYV VSYDIPVETV
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601 DSNLMSHADV IIKGNGLTLS TQAEGLSLQP YEEYLNVVRL VPENFQDFHS
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701 VVAADVEHCE CPQGYGTSC ESCLSGYYRV DGILFGGICQ PCECHGHAAE
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751 CNVHGVCIA C AHNTTGVHCE QCLPGFYGEP SRGTPGDCQP CACPLTIASN
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801 NFSPTCHLND GDEVVCDWCA PGYSGAWCER CADGYYGNPT VPGESCVPCD
=====
851 CSGNVDPSEA GHCDSVTGE C LKCLGNTDGA HCERCADGFY GDAVTAKNCR
=====
901 ACECHVKGS H SAVCHLETGL CDCKPNVTGQ QCDQCLHGYY GLDSGHGCRP
=====
951 CNCSVAGSVS DGCTDEGQCH CVPGVAGKRC DRCAHGFYAY QDGSCTPCDC
=====
1001 PHTQNTCDPE TGECCVCPPHT QGGKCEEDED GHWGYDAEVG CQACNCNSLVG
=====
1051 STHHRCDVVT GHCKQCKSKFG GRACDQCSLG YRDPDCVPC DC DLLRGTS GD
=====
1101 ACNLEQGLCG CVEETGACPC KENVFGPQCN ECREGTFALR ADNPLGCSPC
=====
1151 FCSGLSHLCS ELEDYVRTPV TLGSDQPLLR VVSQSNNLRGT TEGVYYQAPD
=====
1201 FLLDAATVRQ HIRAEFPFYWR LPQQFQGDQL MAYGGKLKYS VAFYSLDGVG
=====
1251 TSNFEPQVLI KGGRIRKQVI YMDAPAPENG VRQEAEVAMR ENFWKYFNSV
=====
1301 SEKPVTREDF MSVLSDIEYI LIKASYGQGL QQRISDISV EVGRKAEKLH
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1351 PEEEVASLLE NCVCPPGTVG FSCQDCAPGY HRGKL PAGSD RGPRPLVAPC
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1401 VPCSCNNHSD TCDPNTGKCL NCGDNTAGDH CDVCTS GYYG KVTGSASDCA
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1451 LCACPHSPPA SFSPTCVLEG DHDFRCDACL LGYEGKH CER CSSYYGNPQ
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1501 TPGGSCQKCD CNRHGSVHGD CDRTSGQCVC RLGASGLRCD ECEPRHILME
=====
1551 TDCVSCDDEC VGVLNLNLD E IGDAVLSLNL TGIIPV PYGI LSNLENTTKY
=====
1601 LQESLLKENM QKDLGKIKLE GVAEETDNLQ KKLTRMLAST QKVNRATERI
=====
1651 FKESQDLAVA IERLQMSITE IMEKTTLNQT LDED FLLPNS TLQNM QQNGT
=====
1701 SLLEIMQIRD FTQLHQ NATL ELKAAEDLLS QIQENYQKPL EELEV LKEAA
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1751 SHVLSKHNNE LKAAEALVRE AEA KMQESNH LLLMVNANLR EFSDKKLHVQ
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=====
1801 EEQNLTSELI VQGRGLIDAA AAQTDAVQDA LEHLEDHQDK LLLWSAKIRH
=====
1851 HIDDLVMHMS QRNAVDLVYR AEDHATEFQR LADVLVYSGLE NIRNVSLNAT
=====
1901 SAAYVHYNIQ SLIEESEELA RDAHRTVTET SLLSESLSVN GKAAVQRSSR
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1951 FLKEGNLNSR KLPGIALELS ELRNKTNRFQ ENAVEITRQT NESLLILRAI
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2001 PEGIRDKGAK TKELATSASQ SAVSTLRDVA GLSQELLNTS ASLSRVNTTL
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2051 RETHQLLQDS TMATLLAGRK VKDVEIQANL LFDRLKPLKM LEENLSRNLS
=====
2101 EIKLLISQAR KQAASIKVAV SADRDCIRAY QPQISSTNYN TLTLNVKTQE
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2151 PDNLLFYLGGS STASDFLAVE MRRGRVAFLW DLGGSGSTRLE FPDFPIDNR
=====
2201 WHSIHVAREFG NIGSLSVKEM SSNQKSPTKT SKSPGTANVL DVNNSTLMFV
=====
2251 GGLGGQIKKS PAVKVTHFKG CLGEAFLNGK SIGLWNYIER EGKCRGCFGs
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2301 SQNEDPSFH DGSGYSVVEK SLPATVTQII MLFNTFSPNG LLLYLGSYGT
=====
2351 KDFLSIELFR GRVKVMTDLG SGPITLLTDR RYNNGTWYKI AFQRNRKQGV
=====
2401 LAVIDAYNTS NKETKQGETP GASSDLNRLD KDPIYVGGLP RSRVVRRGVT
=====
2451 TKSFVGCIKN LEISRSTFDL LRNSYGVRKG CLLEPIRSVS FLKGGYIELP
=====
2501 PKSLSPESEW LVTFATTNSS GIILAALGGD VEKRGDREEA HVPFFSVMLI
=====
2551 GGNIEVHVNP GDGTGLRKAL LHAPHTGTCSD GQAHSISLVR NRRIITVQLD
=====
2601 ENNPVEMKLG TLVESRTINV SNLYVGGIPE GEGTSLLTMR RSFHGCIKNL
=====
2651 IFNLELLDFN SAVGHEQVDL DTCWL SERPK LAPDAEDSKL LREPRAFP EQ
=====
2701 CVVDAALEYYV PGAHQFGLTQ NSHFILPFNQ SAVRKKLSVE LSIRTFASSG
=====
2751 LIYYMAHQNQ ADYAVLQLHG GRLHFMFDLG KGRTKVSHPA LLSDGKWHTV
=====
2801 KTDYVKRKG ITVDGRESPM VTVVGDGTML DVEGLFYLG LPSQYQARKI
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2851 GNITHSIPAC IGDVTVNSKQ LDKDSPVSAF TVNRCYAVAQ EGTYFDGSGY
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2901 AALVKEGYKV QSDVNITLEF RTSSQNGVLL GISTAKVDAI GLELVDGKVL
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2951 FHVNNAGRI TPAYEPKTAT VLCDGKWHTL QANKSKHRIT LIVDGNAVGA
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3001 ESPHTQSTSV DTNNPIYVGG YPAGVKQKCL RSQTSFRGCL RKLALIKSPQ
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3051 VQSFDFSRAF ELHGVFLHSC PGTEs
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HITS AT: 1-3075

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

DT.CA Cplus document type: Journal; Patent

RL.P Roles from patents: BIOL (Biological study); PROC (Process); PRP

Rooke 10/015, 956

(Properties); USES (Uses)  
RL.NP Roles from non-patents: PRP (Properties)  
2 REFERENCES IN FILE CA (1907 TO DATE)  
2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> d 150 sqide 1-58  
YOU HAVE REQUESTED DATA FROM FILE 'REGISTRY' - CONTINUE? (Y)/N:y

L50 ANSWER 1 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN **482390-90-9** REGISTRY

CN Green fluorescent protein [65-glycine,72-alanine,203-tyrosine] (Aequorea victoria) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPVPWPTL VTTFGYGVQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSYQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study); PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 2 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN **481774-46-3** REGISTRY

CN Green fluorescent protein [65-glycine,68-leucine,72-alanine] (Aequorea victoria) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPVPWPTL VTTFGYGLQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 3 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 481774-45-2 REGISTRY

CN Green fluorescent protein [65-glycine,68-leucine,72-alanine,148-glycine,203-tyrosine] (Aequorea victoria) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== 51 GKLPVPWPTL VTTFGYGLQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== 101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSSNV  
===== 151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== 201 LSYQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
=====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 4 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 481774-44-1 REGISTRY

CN Green fluorescent protein [65-glycine,72-alanine,203-tryptophan] (Aequorea victoria) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== 51 GKLPVPWPTL VTTFGYGVQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== 101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== 151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== 201 LSWQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
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HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA CAplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 5 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-43-0 REGISTRY  
CN Green fluorescent protein [65-glycine,68-leucine,69-lysine,72-alanine,203-tyrosine] (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== 51 GKLPVPWPTL VTTFGYGLKC FARYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== 101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== 151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== 201 LSYQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
=====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA CAplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 6 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-42-9 REGISTRY  
CN yGreen fluorescent protein [65-leucine,65-glycine,72-alanine,203-tyrosine] (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== 51 GKLPVPWPTL VTTFGYGVQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== 101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== 151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== 201 LSYQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
=====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA CAplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 7 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 481774-41-8 REGISTRY

CN Green fluorescent protein [65-threonine,203-tyrosine] (Aequorea victoria)  
(9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 238

SEQ 1 MSKGEEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPVPWPPTL VTTFTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSYQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA CAplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 8 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 481774-40-7 REGISTRY

CN Green fluorescent protein [65-threonine,203-histidine] (Aequorea victoria)  
(9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 238

SEQ 1 MSKGEEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPVPWPPTL VTTFTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSHQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 9 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-39-4 REGISTRY  
CN Green fluorescent protein [72-alanine,145-phenylalanine,203-leucine]  
(Aequorea victoria) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN Sapphire protein (Aequorea victoria mutant)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPPWPPTL VTTFSYGVQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNFNSHNV  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
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201 LSLQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
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HITS AT: 1-238  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 10 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-38-3 REGISTRY  
CN Green fluorescent protein [65-glycine,72-alanine,79-arginine,203-tyrosine]  
(Aequorea victoria) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN Topaz protein (Aequorea victoria mutant)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPPWPPTL VTTFGYGVQC FARYPDHMRR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSQYSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== =====

HITS AT: 1-238  
MF Unspecified

CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA CAplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 11 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-37-2 REGISTRY  
CN Green fluorescent protein [66-tryptophan] (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== 51 GKLGPVPWPTL VTTFSWGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== 101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== 151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQQNTPIGD GPVLLPDNHY  
===== 201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
=====

HITS AT: 1-238  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA CAplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 12 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-36-1 REGISTRY  
CN Green fluorescent protein [66-phenylalanine] (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== 51 GKLGPVPWPTL VTTFSFGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== 101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== 151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQQNTPIGD GPVLLPDNHY  
===== 201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
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HITS AT: 1-238  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA CAplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 13 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN **481774-35-0** REGISTRY  
CN Green fluorescent protein [65-leucine] (Aequorea victoria) (9CI) (CA  
INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPVPWPTL VTTFLYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 14 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN **481774-34-9** REGISTRY  
CN Green fluorescent protein [65-cysteine] (Aequorea victoria) (9CI) (CA  
INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPVPWPTL VTTFCYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 15 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN **481774-33-8** REGISTRY  
CN Green fluorescent protein [54-alanine] (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLAAPWPPTL VTTFSYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
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===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
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201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
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HITS AT: 1-238

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 16 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN **481774-32-7** REGISTRY  
CN Green fluorescent protein [64-leucine,65-threonine] (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPPWPPTL VTTLTGYVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)

Rooke 10/015, 956

. 1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 17 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-31-6 REGISTRY  
CN Green fluorescent protein [65-threonine,72-alanine,149-lysine,153-threonine,167-threonine] (Aequorea victoria) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN Emerald protein (Aequorea victoria mutant)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== 51 GKLPVPWPPTL VTTFTYGVQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== 101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHKV  
===== 151 YITADKQKNG IKVNFKTRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== 201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
=====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 18 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-30-5 REGISTRY  
CN Green fluorescent protein [65-threonine,153-alanine,238-glutamic acid]  
(Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== 51 GKLPVPWPPTL VTTFTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== 101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== 151 YIAADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== 201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYE  
=====

HITS AT: 1-238

MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)

Rooke 10/015, 956

1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 19 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN **481774-29-2** REGISTRY  
CN Green fluorescent protein [64-leucine,65-threonine,66-tryptophan,146-  
isoleucine,153-threonine,163-alanine] (Aequorea victoria) (9CI) (CA INDEX  
NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPVPWPPTL VTTLTWGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYISHNV  
===== ===== ===== ===== =====  
151 YITADKQKNG IKANFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

MF Unspecified  
CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 20 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN **481774-28-1** REGISTRY

CN Green fluorescent protein [65-alanine,66-tryptophan,72-alanine,146-  
isoleucine,153-threonine,163-alanine] (Aequorea victoria) (9CI) (CA INDEX  
NAME)

FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPVPWPPTL VTTFAWGVQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYISHNV  
===== ===== ===== ===== =====  
151 YITADKQKNG IKANFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

MF Unspecified  
CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 21 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-27-0 REGISTRY  
CN Green fluorescent protein [66-tryptophan,123-valine,145-histidine,148-arginine,153-threonine,163-alanine,212-lysine] (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== 51 GKLPVPWPTL VTTFSWGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== 101 KDDGNYKTRA EVKFEGDTLV NRVELKGIDF KEDGNILGHK LEYNHNSRNV  
===== 151 YITADKQKNG IKANFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== 201 LSTQSALSKD PKEKRDHMVL LEFVTAAGIT HGMDELYK  
=====

HITS AT: 1-238

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 22 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-26-9 REGISTRY  
CN Green fluorescent protein [66-tryptophan,146-isoleucine,153-threonine,163-alanine,212-lysine] (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== 51 GKLPVPWPTL VTTFSWGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== 101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYISHNV  
===== 151 YITADKQKNG IKANFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== 201 LSTQSALSKD PKEKRDHMVL LEFVTAAGIT HGMDELYK  
=====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

Rooke 10/015, 956

L50 ANSWER 23.OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN **481774-25-8** REGISTRY  
CN Green fluorescent protein [66-histidine,145-phenylalanine,163-alanine]  
(Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ        1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== ===== =====  
      51 GKLPVPWPTL VTTFSHGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== ===== =====  
    101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNFNSHN  
===== ===== ===== ===== ===== =====  
   151 YIMADKQKNG IKANFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNH  
===== ===== ===== ===== ===== =====  
  201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
      1 REFERENCES IN FILE CA (1907 TO DATE)  
      1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 24 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN **481774-24-7** REGISTRY  
CN Green fluorescent protein [66-histidine,145-phenylalanine] (Aequorea  
victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ        1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== ===== =====  
      51 GKLPVPWPTL VTTFSHGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== ===== =====  
    101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNFNSHN  
===== ===== ===== ===== ===== =====  
   151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNH  
===== ===== ===== ===== ===== =====  
  201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
      1 REFERENCES IN FILE CA (1907 TO DATE)  
      1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 25 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN **481774-23-6** REGISTRY

Rooke 10/015, 956

CN Green fluorescent protein [66-histidine] (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== ===== =====  
51 GKLPVPWPTL VTTFSHGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== ===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== ===== =====  
201 LSTQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 26 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-22-5 REGISTRY  
CN Green fluorescent protein [65-glycine,68-leucine,72-alanine,148-glutamine,203-tyrosine] (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== ===== =====  
51 GKLPVPWPTL VTTFGYGLQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSQNV  
===== ===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== ===== =====  
201 LSYQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 27 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-21-4 REGISTRY

Rooke 10/015, 956

CN Green fluorescent protein [65-glycine,68-leucine,72-alanine,203-tyrosine]  
(Aequorea victoria) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN Yellow fluorescent protein (Aequorea victoria mutant)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPVPWPPTL VTTFGYGLQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSYQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA CAplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 28 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 481774-20-3 REGISTRY

CN Green fluorescent protein [65-threonine] (Aequorea victoria) (9CI) (CA  
INDEX NAME)

FS PROTEIN SEQUENCE

SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT  
===== ===== ===== ===== =====  
51 GKLPVPWPPTL VTTFTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY  
===== ===== ===== ===== =====  
201 LSTQQSALSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA CAplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 29 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-19-0 REGISTRY  
CN Green fluorescent protein [endo-1a-valine,65-glycine,72-alanine,203-tyrosine] (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 239

SEQ 1 MVSKGEEELFT GVVPILVLED GDVNGHKFSV SGELEGDATY GKTLKFICT  
===== ===== ===== ===== =====  
51 TGKLPVPWPPT LVTTFGYGVQ CFARYPDHMK RHDFFKSAMPE EGYVQERTIF  
===== ===== ===== ===== =====  
101 FKDDGNYKTR AEVKFEGDTL VNRIELKGID FKEDGNILGH KLEYNNSHN  
===== ===== ===== ===== =====  
151 VYIMADKQKN GIKVNFKIRH NIEDGSVQLA DHYQQNTPIG DGPVLLPDNH  
===== ===== ===== ===== =====  
201 YLSYQSALSK DPNEKRDHMV LLEFVTAAAGI THGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-239  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent  
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study); PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 30 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 481774-18-9 REGISTRY  
CN Green fluorescent protein (Aequorea victoria) (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 238

SEQ 1 MSKGEEELFTG VVPILVELDG DVNGHKFSVS GELEGDATYG KLTLKFICCT  
===== ===== ===== ===== =====  
51 GKLKPVPWPPTL VTTFSYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF  
===== ===== ===== ===== =====  
101 KDDGNYKTRA EVKFEGDTLV NRRIELKGIDF KEDGNILGHK LEYNNSHN  
===== ===== ===== ===== =====  
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNH  
===== ===== ===== ===== =====  
201 LSTQQSALSKD PNEKRDHMVL LEFVTAAAGIT HGMDELYK  
===== ===== ===== ===== =====

HITS AT: 1-238

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL  
DT.CA Cplus document type: Patent  
RLD.P Roles for non-specific derivatives from patents: ANST (Analytical study); BIOL (Biological study); PREP (Preparation); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 31 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 325868-75-5 REGISTRY  
 CN Protein No55 (human DU145 cell cell nucleolus-associated gene No55) (9CI)  
 (CA INDEX NAME)  
 OTHER NAMES:  
 CN GenBank CAC16786  
 CN GenBank CAC16786 (Translated from: GenBank AJ250583)  
 CN Nucleolar protein No55 (human DU145 cell gene No55)  
 FS PROTEIN SEQUENCE  
 SQL 437

SEQ        1 MARVAWGLLW LLLGSAGAQY EKYSFRGFPP EDLMPLAAAY GHALEQYEGER  
 =====  
 51 SWRESARYLE AALRLHRLR DSEAFCHAN C SGPA PAAKPD PDGGRADEWA  
 =====  
 101 CELRLFGRVL ERAACLRRCK RTLPAFQV PY PPRQLLRDFQ SRLPYQYLHY  
 =====  
 151 ALFKANRLEK AVAAAYTFLQ RNPKHELTAK YLNYYRGMLD VADES LTDLE  
 =====  
 201 AQPYEAVFLR AVKLYNSGDF RSSTEDMERA LSEYLA VFAR CLAGCEGAHE  
 =====  
 251 QVDFKDFYPA IADLFAESLQ CKVDCEANLT PN VGGYFVDK FVATMYHYLQ  
 =====  
 301 FAYYKLNDVR QAARSAASYM LFDPKDSVMQ QNLVYYRFHR ARWGLEEEDF  
 =====  
 351 QPREEAMLYH NQTAELRELL EFTHMYLQSD DEMELEETEP PLEPEDALSD  
 =====  
 401 AEFEGE GEDYE EGMYADWWQE PDAKGDEAEA EPEPELA  
 =====

HITS AT: 1-437

MF Unspecified  
 CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA CAPplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)  
 1 REFERENCES IN FILE CA (1907 TO DATE)  
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 32 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 296363-99-0 REGISTRY  
 CN G-protein coupled receptor VLGR1 (human precursor) (9CI) (CA INDEX NAME)  
 OTHER NAMES:  
 CN GenBank AAD55586  
 CN GenBank AAD55586 (Translated from: GenBank AF055084)  
 CN Very large G-protein coupled receptor-1 (human precursor)  
 FS PROTEIN SEQUENCE  
 SQL 1967

SEQ        1 MQLCIFCCCC ILFYFDLYDF GRGYDFTIQE NGLOIDQPPE IGNISIVRII  
 =====  
 51 IMKNDNAEGI IEFDPKYTA F EVEEDVGLIM IPVVR LHGTY GYVTADFISQ  
 =====  
 101 SSSASP GGV D YIHGSTVTF QHGQNLSFIN ISI IDNESE FEEPIEILLT  
 =====  
 151 GATGGAVLGR HLVSRIIIAK SDSPFGVIRF LNQSKISIAN PNSTMILSLV  
 =====  
 201 LERTGGLLGE IQVNWETVGP NSQEALLPQN RDIADPVSGL FYFGE GEGGV  
 =====  
 251 RTIILT IYPH EEIEVEETFI IKLHLVKGEA KLD SRAKDVT LTIQEFGDPN  
 =====

301 GVVQFAPETL SKKTYSEPLA LEGPLLITFF VRRVKGTFGE IMVYWELSSE  
 =====  
 351 FDITEDFLST SGFFTIADGE SEASFDVHLL PDEVPEIEED YVIQLVSVEG  
 =====  
 401 GAELDLEKSI TWFSVYANDD PHGVFALYSR QOSILIGQNL IRSIQINITR  
 =====  
 451 LAGTFGDVAV GLRISSDHKE QPIVTENAER QLVVKDGATY KVDVVPIKNQ  
 =====  
 501 VFSLSGSNT LQLTVMLVG GRFYGMPTIL QEAKSAVLPV SEKAANSQVG  
 =====  
 551 FESTAFQLMN ITAGTSHVMI SRRGTYGALS VAWTGTYAPG LEIPEFIVVG  
 =====  
 601 NMTPTLGSLS FSHGEQRKGV FLWTFPSPGW PEAFVLHLSG VQSSAPGGAQ  
 =====  
 651 LRSGFIVAEI EPMGVFQFST SSRNIIVSED TQMIRLHVQR LFGFHSDLIK  
 =====  
 701 VSYQTTAGSA KPLEDFEPVQ NGELFFQKFQ TEVDFEITII NDQLSEIEEF  
 =====  
 751 FYINLTSVEI RGLQKFDVNW SPRLNLDHSV AVITILDNDD LAGMDISFPE  
 =====  
 801 TTVAVAVADTT LIPVETESTT YLSTSCTTTI LQPTNVVAIV TEATGVSAIP  
 =====  
 851 EKLVTLHGTP AVSEKPDVAT VTANVSIHGT FSLGPSIVYI EEEMKNGTFN  
 =====  
 901 TAEVLIRRRTG GFTGNVSITV KTFGERCAQM EPNALPFRGI YGISNLTWAV  
 =====  
 951 EEEEDFEEQTL TLIFLDGERE RKVSVQILDD DEPEGQEFFFY VFLTNPQGGA  
 =====  
 1001 QIVEGKDDTG FAAFAVMVIT GSDLHNGIIG FSEESQSGL LREGAVMRRL  
 =====  
 1051 HLIVTRQPNR AFEDVKVFWR VTLNKTVVVL QKDGVNLME LQSVSGTTTC  
 =====  
 1101 TMGOTKCFIS IELKPEKVPQ VEVYFFVELY EATAGAAINN SARFAQIKIL  
 =====  
 1151 ESDESQSLVY FSVGSRLLAVA HKKATLISLQ VARDSGTGLM MSVNFSTQEL  
 =====  
 1201 RSAETIGRTI ISPAISGKDF VITEGTLVFE PGQRSTVLDV ILTPETGSLN  
 =====  
 1251 SFPKRFQIVL FDPKGARID KVYGTANITL VSDADSQAIW GLADQLHQPV  
 =====  
 1301 NDDILNRVLH TISMKVATEN TDEQLSAMMH LIEKITTEGK IQAFSVASRT  
 =====  
 1351 LFYEILCSLI NPKRKDTRGF SHFAEVTFN AFSLLTNVTC GSPGEKSHTI  
 =====  
 1401 LDSCPYLSIL ALHWYPQQIN GHKFEGKEGD YIRIPERLLD VQDAEIMAGK  
 =====  
 1451 STCKLVQFTE YSSQQWFISG NNLPTLKNKV LSLSVKGQSS QLLTNDNEVL  
 =====  
 1501 YRIYAAEPRI IPQTSLCLLW NQAAAASLSD SQFCKVIEET ADYVECACSH  
 =====  
 1551 MSVYAVYART DNLSYYNEAF FTSGFICISG LCLAVLSHIF CARYSMFAAK  
 =====  
 1601 LLTHMMMAASL GTQILFLASA YASPLAEECS CSAMAAVTHY LYLCQFSWML  
 =====  
 1651 IQSVNFWYVL VMNDEHTERR YLLFFLLSWG LPAFVVILLI VILKGIYHQS  
 =====  
 1701 MSQIYGLIHG DLCFIPNVYA ALFTAALVPL TCLVVVFVVF IHAYQVKPOW  
 =====  
 1751 KAYDDVFRGR TNAAEIPLIL YLFALISVTW LWGGLHMYR HFWMLVLFVI  
 =====

1801 FNSLQGLYVF MVYFILHNQM CCPMKASYTV EMNNGHPGPST AFFTSGSGMP  
 =====  
 1851 PAGGEISKST QNLIGAMEEV PPDWERASFQ QGSQASPDLK PSPQNGATFP  
 =====  
 1901 SSGGYGQGSL IADEESQEFD DLIFALKTGA GLSVSDNESG QGSQEGGTLT  
 =====  
 1951 DSQIVELRRI PIADTHL  
 =====

HITS AT: 1-1967

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 33 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290872-78-5 REGISTRY

CN RTX toxin RtxA (Vibrio cholerae strain N16961 gene VC1451) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF94608

CN GenBank AAF94608 (Translated from: GenBank AE004223)

FS PROTEIN SEQUENCE

SQL 4558

NTE

type	-----	location	-----	description
uncommon	Aaa-3773	-	-	
uncommon	Aaa-3940	-	-	
uncommon	Aaa-3948	-	-	

SEQ 1 MVFYLIPKRR VWLMGKPFWR SVEYFFTGNV SADDGNNNIV AIGFGGQIHA  
 =====  
 51 YGGDDHVTVG SIGATVYTGS GNDTVVGGSA YLKVEDSTGH LIVKGAAAGYA  
 =====  
 101 DINKSGDGNV SFAGAAGGVS IDHLGNHGDV SYGGAAYNG ITRKGLSGNV  
 =====  
 151 TFAGAGGYNA LWHETNQGNL SFTGAGAGNK LDRTWSNRYQ GSHGDVTFDG  
 =====  
 201 AGAANSISSL VETGNITFRG AGADNHVLRK GKVGDIRLQG AGASNRIERT  
 =====  
 251 HQAEDVYTQT RGNIRFEGVG GYNNSLYSDVA HGDIHFSGGG AYNTIIRKGS  
 =====  
 301 GNDFAKEGMT NAKADEIVLT KAVMSGSWIG QDHHTAVKS ASEPNLYLFA  
 =====  
 351 FADSTYTKIN KVQLRNDPQT GELKYYSTAW YKEVNHLSNL ANQDISDNGG  
 =====  
 401 FTAVNINGAY TLSDLKVEHQ QSXTVHHAVEK SLTEYEWVTY ANGAVIDAKE  
 =====  
 451 VSLSDAKMGG HAIYADGTKV DVKAVKSNRQ PNTYIYAKVL GPYTKIVVVE  
 =====  
 501 LANDPETGAL KYQARSWYKE GDHTANIANQ DISSATGYNP MGKGGYSLSD  
 =====  
 551 LHYSVNAVRS TSETVADIEE YTDQTLFKPA NDSESSGDV RFNGAGGGNV  
 =====

601 IKSNVTRGNV HFNGGGIANV ILHSSQFGNT EFNGGGAANV IVKSGEEGDL  
 =====  
 651 TFRGAGLANV LVHQSEQGKM DVYAGGAVNV LVRLGDGQYL AHLLAYGNIS  
 =====  
 701 VQKGSGDSRV VMLGGYNHT QIGSGNGLWL AAGGFNVMTQ VGKGDVAABL  
 =====  
 751 AGGANVLTKM GEGETSGML GGANVITHIS NDDQLSNTTA VALGGANILT  
 =====  
 801 KKGKGNTLAV MGGGANVLTH VGDGTTGVM VGGANILTKV GNGDTTGILL  
 =====  
 851 GVGVLTHVG DGQTLGVMGA AGNIFTKVGD GTSIAVMIGA GNIFTHVGEG  
 =====  
 901 NAWALMGGLG NVFTKVGNGD ALALMVAEAN VFTHIGDGMS VALMLAKGNV  
 =====  
 951 ATKVGNGTTL AAMVGVNIF THIGHGSTFA AMIQQANIMT KVGNDLTAAL  
 =====  
 1001 MVGKANIMTH VGDGTSLGLF AGEVNVMTKV GNGTTLAAMF GKANIMTHVG  
 =====  
 1051 DGLTVLALG EANIVTKLGD DFMGVVAAAK ANVVTHVGDA TAAVLAGKG  
 =====  
 1101 NILTKVGEGET TVGLLISDVG NVMTHVGDGT TIGIAKGKAN LITKVGDGGLG  
 =====  
 1151 VNVTWGQANV FTQVGDGDRY NFAKGEANLI TKVGDGQEVS VVQGEANIIT  
 =====  
 1201 HVGNDDYTG AWGKANVITK VGHGQNVVLA KGEANIVTQV GDGDSFNALW  
 =====  
 1251 SKGNIVTKVG DGMQVTAAKG QANITTTVGN GLNVTAAYGD ANINTKVGDG  
 =====  
 1301 VSVNVAWGKY NINTKVGDGL NVAVMKGKAN ANIHVGDGLN INASYAQNNV  
 =====  
 1351 AIKVGNGDFY SLAVASSNTS SNKLSALFDN IKQTVLGVGG SQAINYLVQG  
 =====  
 1401 DEASSSGTHK GRGAIATPEI TKLDGFQMDA IKEVSSDLGD SLTGSVTKVD  
 =====  
 1451 TPDLNMQHA LNVDDSSVQA PNLLVNGDFE LGEHWQSTH GVEASYAGSV  
 =====  
 1501 YGVEGEGHGA RVTELDTYTN TSLYQDLANL AQGEVIAVSF DFAKRAGLSN  
 =====  
 1551 NEGIEVLWNG EVVFSSSGDE SAWQQKNLKL TAQAGSNRIE FKGTGHNDGL  
 =====  
 1601 GYILDNVVAT SESSQQANAI REHATQNPAQ QNALSDKERA EADRQRLEQE  
 =====  
 1651 KQKQLDAVAG SQSQLESTDQ QALENNQQAQ RDAVKEESEA VTAELAKLAQ  
 =====  
 1701 GLDVLDGQAT HTGESGDQWR NDFAGGLLDG VQSOLDDAKQ LANDKIAAK  
 =====  
 1751 QTLDNNNSKV KESVAKSEAG VAQGEQNrag VEQDIADAQA DAEKRKADAL  
 =====  
 1801 AKGKDAQQAE SDAHHAVNNA QSRGDRDVQ AENKANQAQ DAQGAKQNEG  
 =====  
 1851 DRPDRQGVGTG SGLSGNAHSV EGAGETDSHV NTDSQTNADG RFSEGLTEQE  
 =====  
 1901 QEALEGATNA VNRLQINAGI RAKNSVSSMT SMFSETNSKS IVVPTKVSPE  
 =====  
 1951 PERQEVTRRD VRISGVNLES LSAVQGSQPT GQLASKSPVG FKSHFASTSI  
 =====  
 2001 GIENELSGLV VVLPKNSAQT FGYVHDSQGN PLFMLTKDMN QGGYSNPVGI  
 =====  
 2051 NDIQGVNNWQ THTIELVTYP SEISDTAAVE SRKEAMLWLA KEFTDHINQS

2101 NHQSLPHLVS DDGRFTLVIS NSKHLIAAGN GTSIDAQGKT IGMTPSGQQA  
 =====  
 2151 TMAISAKEFG TSSSPEVRL ESAPWYQAGL RDEFLANAKN TTLDDPATAQ  
 =====  
 2201 NVYAYLTSVY SKTADLAKEY GIYINDWDPA SEGFSPPNAQG LTDPKVNAW  
 =====  
 2251 SILPRTKPVR MLELLSAEDS RYVRQQIAEK LKGTYSES LA KNVFEYFQYG  
 =====  
 2301 GEVAGHGINN ATTGSVQQPE PAILFEFRSV PSALSDFVPK TASTVKVDVK  
 =====  
 2351 ALDHFDASR KAIITEVNAL VSGSEDFDAW YQEYRASKGQ PPVKNPKSSA  
 =====  
 2401 SANHKAEWLM TQHAEQWAKI TAPYTDNHET LTSTKLASND KEELHALGET  
 =====  
 2451 SNLENNKQOE NVASIINTML NDMLPFYALR TERNLVQEG DEGFEVRAWP  
 =====  
 2501 GTEDKSktII LEDPEDAAQH KAIERFILAN FDNFEQMPDE LFLVDNKVIS  
 =====  
 2551 HHEGRTHVLA QKVDGAWQYN ATVELMSVTE LLDAANVTGK IRGESYQQVI  
 =====  
 2601 DALTDYHASI TEHADYEPEs VEKLLNLRKK IEGYVLGHPD SGRVEAMNSL  
 =====  
 2651 LNQVNTRLDE VSLLSVAEQT IQAQNSFSRL YDQLEAANLK ESKHLYLDQN  
 =====  
 2701 GDFVTKGKGN LANIDLLGSR EAVLEKVKLT VSNEYGQTVA DTIFAGLSAK  
 =====  
 2751 DLAKDGKGVD IAGLNKvhQA IEQHLSPVSA TLYIWKPSDH SALGHAALQI  
 =====  
 2801 GQGRtQLEGQ AAADFNFQQNY VSWWPLGSKS SNISNILNVA TKDQPDLKLR  
 =====  
 2851 WSDFSQPAHQ NDTLEHDVAS EENDGFGLHD GDIKLKRFIE KLNAAKGIDA  
 =====  
 2901 SFKEASEGYA SVLLGNPDML ETTSIPAHVF QPFVEQWNDT SYDMMDVAHR  
 =====  
 2951 FAQELRLQAO RSDDPELLEK RIGNVIRQFA ERALEEIEFT KASQADQGRV  
 =====  
 3001 FRINLEGLDV AAMQAEWHRL SNDPDARYQL LTKNCSTVA KVLKAGGADK  
 =====  
 3051 LIGHTWLPKF GVWTPTELFN FGQALQEAEQL EIAAKKQSHQ VTDVLDALSG  
 =====  
 3101 NEKPKENVAI ENDGTPPRDK ESLSPLTRFL NNELYGDKEA RRKIGEITQT  
 =====  
 3151 LLDHAVEKGE SQKITLQGEA GRLTGYYHQG TAPSEGETSS PSGKVVFLH  
 =====  
 3201 GSGSSAAEEQA SAIRNHYQKQ GIDMLAVNLR GYGESDGGPS EKGLYQDART  
 =====  
 3251 MFNYLVNDKG IDPSNIIIHG YSMGGPIAAD LARYAAQNGQ AVSGLLLDRP  
 =====  
 3301 MPSMTKAITA HEVANPAGIV GAIAKAVNGQ FSVEKNLEGL PKETSILLT  
 =====  
 3351 DNEGLGNEGE KLRTKLTASG YNVTGEQTFY GHEASNRLMS QYADQIVSGL  
 =====  
 3401 SSSASVDEDL DQQGLDTTST KDQGISNKND HLQVVDsKEA LADGKILHNQ  
 =====  
 3451 NVNSWGPITV TPTTDGGETR FDGQIIVQME NDPVVAKAAA NLAGKHAESS  
 =====  
 3501 VVVQLDSDGN YRVVYGDPSK LDGKLWRQLOV GHGRDHSETN NTRLSGYSAD  
 =====  
 3551 ELAVKLAKFQ QSFNQAENIN NKPDHISIVG CSLVSDDKQK GFGHQFINAM  
 =====

3601 DANGLRVDVS VRSSELAVDE AGRKHTKDAN GDWVQKAENN KVSLSWDAQG  
 =====  
 3651 EVVAKDERIR NGIAEGDIDL SRIGVNNVDE PARAGAIGDNN DVFDAPEKRK  
 =====  
 3701 PETEVIANSS SSNQFSYSGN IQNVNGEGEF TAVNWGTSNV GIKVGTGGFK  
 =====  
 3751 SLAFGDNNVM VHIGDGESKH SVXIGGYQAL EGAQMFLGNR NVSFNFHHSN  
 =====  
 3801 DLILMMDKSI PTPPLVNPFD GAARISGVLQ GIATSGEGED WLAAQEQQWT  
 =====  
 3851 LSGAKKFVKD MSGLDQSSSV DYTTLVELDS QNERDSRGLK HDAEATLNKQ  
 =====  
 3901 YNQWLGSNGN SGTSQLSRAD KLRQANEKLA FNFAVGGQGX DIQVTGXWN  
 =====  
 3951 FMFGDNIQSI LDTNLGSLFG LMTQQFTATG QAKTTFTYTP QDLPRQLKNK  
 =====  
 4001 LLGQLAGVGA ETTLADIFGV DYTASGQIVS RNGQAVDGVA ILKEMLEVIG  
 =====  
 4051 EFSGDQLQAF VDPAKLLDSL KAGIDMGADG IKSFAETHGL KEKAPEEEKD  
 =====  
 4101 NSSVSVNGAN VNSAQGATVA DGNTEATAETQ DRAFGFNSLN LPNLFATIFS  
 =====  
 4151 QDKQKEMKSL VENLKQNLTA DLLNMKEKTF DFLRNNSGHLQ GGDGINISLG  
 =====  
 4201 NYNFNWGGDG KDLGAYLGDN NNFWGGRGDD VFYATGKSNI FTGGEGNNDMG  
 =====  
 4251 VLMGRENMME GGDGNDTAVV AGRINHVFLG AGDDQSJVFG EGGEIDTGSG  
 =====  
 4301 RDYVVTSGNF NRVDTGDDQD YSVTIGNNNQ VELGAGNDFA NIFGNYNRIN  
 =====  
 4351 AGAGNDVVKL MGYHAVLNGG DGDDHLLIATA ISKFSQFNNG EGRDLMVLGG  
 =====  
 4401 YQNTFKGGTD VDSFVVSGDV IDNLVEDIRS EDNIVFNGID WQKLWFERSG  
 =====  
 4451 YDLKLSILRD PSNDSDQSKF EHIGSVTFSD YFNGNRAQVV IGMSEKDLSG  
 =====  
 4501 EREYTMMLS AIDALVQAMS GFEPQAGDNG FIDSLESKSQ AAISMAWSDV  
 =====  
 4551 VHKKGLMV  
 =====

HITS AT: 1-4558

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 34 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290417-48-0 REGISTRY

CN 5'-Nucleotidase (Vibrio cholerae strain N16961 gene VCA0545) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF96447

CN GenBank AAF96447 (Translated from: GenBank AE004385)

FS PROTEIN SEQUENCE

SQL 580

SEQ        1 MPMRRKNQPA SITLAHINDT HSYFEPTSLQ LTLEHDADIL KPFVSAGGFA  
 =====  
 51 RIATRIAQLR DDAQRQMREF LFLHAGDCFQ GTLYFSLFKG KANADMLNAL  
 =====  
 101 KLDAMAINNH ELDGMNYPVA QFAAQRIQFPL LAGNWDLSQE RDSKSLRLGS  
 =====  
 151 NPKVYSYDAL QGHARWIEKK AQGERIAIFG LSIDKMADIA NPDSDTPFVN  
 =====  
 201 AIETARKTIA AIHQHGINKI ILLSHLGYDG DIALAEQVSG ISLIVGGHSH  
 =====  
 251 VLQGDFSALG LGSQDEYGLK INHTYIVQAG FYALTLCQ IDFAANGEVT  
 =====  
 301 RFEGRNELLL GRRMFVDASM SQEQISERYS QARDEVNDHP NVVVCKKDPV  
 =====  
 351 VQSLLQEKEYI PQVRQLQQQI IAHADRTLH LRIPDAEGGS EIAPLVAKAF  
 =====  
 401 VYALNKRGGLD VQFAIHNAAGG VRTSILPGSI SVADVAGKLL PFAVPIGVYQ  
 =====  
 451 VKGEVIARAL EGAINNALS N GVQGTGSSY PYCHHLRYQY LADKPIGQRI  
 =====  
 501 TQLQIQLDGE WQAVDSEALY WGTSSAYTMK GKEGYDALLD MEGEGMVTQI  
 =====  
 551 SMADAFIELL SDCPSLLSFE AHDACECHH  
 =====

HITS AT: 1-580

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Cplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 35 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290417-17-3 REGISTRY

CN Protein (Vibrio cholerae strain N16961 gene VCA0510) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF96413

CN GenBank AAF96413 (Translated from: GenBank AE004381)

FS PROTEIN SEQUENCE

SQL 968

SEQ        1 MTHYQTEIGK IMYSSHQCKR LSIMAILGCL PFSVNGAVES MPLMGGVYNS  
 =====  
 51 AHVFKHQITN SLSYSTRLTR DTALFTIAGL TLDSYILTLP LDVKTKARVI  
 =====  
 101 KQISDPSYAI PLGYFLYQYY DRYTGMATED QFKNYLSTVY DEPALKGFEH  
 =====  
 151 SLFQLGKPVV TEQSOHSKDQ AHQEGIKVDS EFIATMVTLY DALVQIGEWR  
 =====  
 201 DLKQLPSQYQ YLSDTPADNA LVSKIQPLVV DILRQTANGM DEGEMKHALL  
 =====  
 251 SVLEDAKPen ANKVNNKAQA ITVSLIDFVR LNVLKGYRQF LYQEERTARL  
 =====  
 301 KEWLNTLDS DPEQLVTFLT SQQQRRFAVQ VTVDGLQQGL IEGLVHPENP  
 =====

```

351 FIKQVYAEHQ QAEKNQHSTL MEPLEHKQQV RFLSTLAEQN YQDPYYLPFF
=====
401 KQLYQHYRQT IVQVGISSTP TISVRNLPII KTGAKVSGLG GTGIPNFHFV
=====
451 DRQADRAYYF FGNDALQLDR LVNERGVKTM FDRLDYLKTL NCNAQYDWNA
=====
501 HTTYDGLVNL GAGEALRDFG EKRCLRELNE RAEERQLTA LRAKLIEQIT
=====
551 AYQNSSKWMV LTRATLKQRL EQQLAHEYAER DIFGMPDYTL IYNPWPDHFA
=====
601 HFAGPFSDEV IMPTGELNRL DYWLRETEAA YKKAGIYERT LWGMAGDHGL
=====
651 APVYGTLNPE RKIFESLQKD LGIKIALEKI SSDEGEKPQ TNALNAPSYQ
=====
701 KIDVVVASTA GGNFMFLDFN SAAGWATQPI YQELTQWQPK ESDKPLDIVS
=====
751 ESLVRLGDSL DYLVVREKTC TVDDCAVRVI GMREGLRLDE IIRLVGNKRF
=====
801 YTSQQGQPQL LQLQQLPYL PKPQANALEE FAQLVDKCLY RAEEANIATW
=====
851 CDEQEWRQLT RFTPRPD SVN QLAALYEEDR AGTMNLFPKQ GVGYNTKVPG
=====
901 RHAGESYLEK DAFLGFWGKP IGPNAMELQS EQNGSLAPTL YEYLTGESIE
=====
951 AGHDGwgypS LLNKLDIQ
===== =====

```

HITS AT: 1-968

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 36 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290415-80-4 REGISTRY

CN Threonyl-tRNA synthetase (Vibrio cholerae strain N16961 gene VCA0287)  
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF96196

CN GenBank AAF96196 (Translated from: GenBank AE004368)

FS PROTEIN SEQUENCE

SQL 642

```

SEQ . 1 MPIITLPDGs QRHFDNPVST LEVAQSIGPG LAKATIAGRv NGARVDACDL
=====
51 IEHDASLEII TTKDEVGLe IvrhscahLL GHalkqlYpn Akmaigptid
=====
101 SGFYyDIDLe QSLsqedLeK iearmvelak tkyavvKKV swqeardtfe
=====
151 SRGESYKMEI LDENVArDDr PGLYHHEEYI DMCRGPHVPh MGFCQNFkll
=====
201 NIAGAYWRGN SDNkmlqriy GTAFHDkkal qahltrLeeA AKRDHRKIGk
=====
251 QLDLFHMQOE APGMVFWhn GWSifrdLeI FIRQKLNEYG YQEVKGplmm
=====
301 DRVLWERSGH WDKYADAMFT TSSENREyAI KPMNCPGHIQ IFNQGLKSYR
===== =====

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351 DLPLRMAEFG SCHRNEPSGS LHGIMVRGF TQDDAHIFCT EDQIQQEVTS  
===== ===== ===== ===== ===== =====  
401 CIKMQVYDTYT TFGFQNIVVK LSTRPEKRVG SDEIWDKSEQ ALIDSLKAMD  
===== ===== ===== ===== ===== =====  
451 IPFEIQEGEG AFYGPKIEFT LYDCLDRAWQ CGTVQLDFNL PTRLGATYVG  
===== ===== ===== ===== ===== =====  
501 ESNERLIPVM IHRAILGSLE RFIGILIEEY AGFFPTWLAP EQAVVVNITD  
===== ===== ===== ===== ===== =====  
551 KQADYAHEVA QKLQKCGIRA KADLRNEKIG FKIREHTLKR VPYMLVCGDQ  
===== ===== ===== ===== ===== =====  
601 EMEAGEIAVR TRKGKDLGKF KLDDFIAHIQ AEIASRKLN L EE  
===== ===== ===== ===== ===== ==

HITS AT: 1-642

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Cplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 37 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290410-83-2 REGISTRY

CN Dehydrogenase; 3-isopropylmalate (Vibrio cholerae strain N16961 gene VC2491) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 3-Isopropylmalate dehydrogenase (Vibrio cholerae strain N16961 gene VC2491)

CN GenBank AAF95633

CN GenBank AAF95633 (Translated from: GenBank AE004318)

FS PROTEIN SEQUENCE

SQL 363

SEQ 1 MTDRDYKIAV LPDGIGPEV MAQAHKVLD A IEQKHGIRFS REEHDVGGIA  
===== ===== ===== ===== ===== =====  
51 IDNHGCPLPE STLRACEEAD AVLFGSVGPG KWEHLPPNEQ PERGALLPLR  
===== ===== ===== ===== ===== =====  
101 KHFQLFCNLR PAQIHQGLEA FSPLRADISA RGFDIVVRE LTGGIYFGQP  
===== ===== ===== ===== ===== =====  
151 KGREGEGAHE KAFDTEVYHR FEIERIARIA FESARLRRKK VCSIDKANVL  
===== ===== ===== ===== ===== =====  
201 QSSILWREVV SEIAKEYPDV SLHMYIDNA TMQLIKDPAQ FDVMLCSNIF  
===== ===== ===== ===== ===== =====  
251 GDILSDECAM ITGSMGLPS ASMNESKFGL YEPAGGSAPD IAGKNIANPV  
===== ===== ===== ===== ===== =====  
301 AQILSAALML RYSLGEEAAA RDIENAVSQA LAAGELTADL AGSKPALSTS  
===== ===== ===== ===== ===== =====  
351 AMGDKIASYI LNS  
===== ==

HITS AT: 1-363

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Cplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

Rooke 10/015, 956

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 38 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 290410-70-7 REGISTRY  
CN Protein (Vibrio cholerae strain N16961 gene VC2476) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN GenBank AAF95618  
CN GenBank AAF95618 (Translated from: GenBank AE004317)  
FS PROTEIN SEQUENCE  
SQL 157

SEQ 1 MLSGGGLSLND KSWQALVFDY TNDGMGWPIG ALASAEQILL AMSAQLVDTD  
===== 51 FELSLLLPEG EGEEALFELA DAVAEGWINHF ISGLGLSGAN LKHASVEAKE  
===== 101 ALEDLEEMSK LGIDEEDDLA EQAELLEQVI EHIKACVLVL HAEFGVKPEQ  
===== 151 DTKPTVH  
=====

HITS AT: 1-157

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Cplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 39 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 290408-81-0 REGISTRY  
CN Elongation factor Ts (Vibrio cholerae strain N16961 gene VC2259) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN GenBank AAF95403  
CN GenBank AAF95403 (Translated from: GenBank AE004297)  
FS PROTEIN SEQUENCE  
SQL 280

SEQ 1 MAVTAALVKE LRERTGAGMM ECKKALVETN GDIELAIENM RKSGAAKA  
===== 51 KAGNIAAEGT IMIKEGEGLA ALVEVNCQTD FVAKDSNFVA FANQVTDAAL  
===== 101 ASKASVEELQ AQFEEARVAL VAKIGENINI RRVQYVEGEA LATYRHGDRI  
===== 151 GVVVAGSADV ETLKHVAMHV AASRPEFLTP DDVPAEVVAK EREVQVGIA  
===== 201 NEGKSKEIAE KMVEGRMKKF TGEVSLTGQP FVMEPKKTVG EILAEKGATV  
===== 251 SAFIRLEVGE GIEKQEGLSF AEEVALAQKG  
=====

HITS AT: 1-280

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Cplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

. 1 REFERENCES IN FILE CA (1907 TO DATE)  
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 40 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
 RN 290407-23-7 REGISTRY  
 CN Peptidase, insulinase family (*Vibrio cholerae* strain N16961 gene VC2072) (9CI) (CA INDEX NAME)  
 OTHER NAMES:  
 CN GenBank AAF95218  
 CN GenBank AAF95218 (Translated from: GenBank AE004281)  
 FS PROTEIN SEQUENCE  
 SQL 939

SEQ        1 MVFCDSSTL PIRRNAVHIS PNDTHQYRYI TLSNGLRTLL IQSPDVQKCA  
 =====  
 51 AALAVNVGHF DDPIERQGLA HYLEHMLFLG TEKYPKVGDF QTFISQHGGS  
 =====  
 101 NNAWTGTEHT CFFFDVLPNA FAKALDRFSQ FFIAPLFNAE ALDKERQAVD  
 =====  
 151 SEYKLKIKDE SRRLYQVQKE TINPQHPFSK FSVGQNQHTLG DRENSSIRDE  
 =====  
 201 IIEFYQSHYS AKLMTLSLIG SQSFDELEAW AERYFAAIPN PQRDIKPLPP  
 =====  
 251 FVDREHTGIL IQIEPLKEIR KLILAFPMPS TESYYQKKPL SYFAHLIGYE  
 =====  
 301 GEGSLLEALK EKGWITTLSA GGGVSGSNYR EFAVSCVLTQ EGLDHVDEII  
 =====  
 351 QSLFQTTLNLI ATQGLQAWRY QEKRAVLESA FRFQETQRPL DMVSHLVVNM  
 =====  
 401 QHYAPEDTAY GDYMMMSGYDE ALLLHILSYL TPENLRATLI AKGGEYDKKA  
 =====  
 451 QWYFTPYSVR PFTTEQLHRF RQPLDLPISL PEPNPFCYD LDPSEVKESH  
 =====  
 501 TLPQVLQDLP GFKLWHQQDT EFRVPKGVIY VAIDSPHAVA NCRNIVMTRL  
 =====  
 551 CVEMFLDALA KETYQAEIAG MGYNLYAHQG GVTTLTSGFS QKLPQLMEVI  
 =====  
 601 LRKFAQRDFQ PKRFATIKQQ MTRNWRNAAH DKPISQLFNA MTGLLQPNNP  
 =====  
 651 PYAELLAAID DVQVEELAHF VDTILSQLHV EMFVYGDWPA AEAHKMAEVL  
 =====  
 701 KDALRVQGQT YEESLRPLVM LGKSGTFQRE VQCQQDDSAI VVYYQSHEVS  
 =====  
 751 PRSIALYSLA NHLMSATFFH EIRTKQQLGY MVGTGNMPLN RHPGLILYVQ  
 =====  
 801 SPSAPPSELI RSIDEFLNAL YMVLLELNEY QWHSSKRGLW NQISAPDPTL  
 =====  
 851 RIRAQRLWVA IGNKDLSFDQ REKVLEELKN LSRADMIRFV VNELKPRTAH  
 =====  
 901 RLIMHTQGRA HHEAPALQLG QEIGSVEEFQ LRPKAYDVG  
 =====

HITS AT: 1-939

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

. 1 REFERENCES IN FILE CA (1907 TO DATE)

. 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 41 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 290404-95-4 REGISTRY  
CN Sigma-54 dependent transcriptional regulator (*Vibrio cholerae* strain N16961 gene VC1817) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN GenBank AAF94965  
CN GenBank AAF94965 (Translated from: GenBank AE004257)  
FS PROTEIN SEQUENCE  
SQL 587

SEQ        1 MMQLQQQLSHV NWLVNSWQRS EQAGLTQQSR AQDIRLSDNK LKERRQELAG  
===== ===== ===== ===== ===== =====  
      51 LIDTVSRFAL PLFYQLFAHS DSRLILTDQH GVIIGSWGQA RFREKLSQIA  
===== ===== ===== ===== ===== =====  
    101 LSSGACWQEP IKGTNAIGTA LIEQKPIISVI GEQHFIQHHH FISCSASPIF  
===== ===== ===== ===== ===== =====  
   151 DYTGQLIGVL DITSEQQKHT LSTQVVVQNM VQLVENQLLN QIPHGHVRID  
===== ===== ===== ===== ===== =====  
  201 LACEPSLLSS GWQGVIIADE SGQILAHNQV AGQLLAQGRV IGQSVEQVLP  
===== ===== ===== ===== ===== =====  
251 RPQTHASFIY TTTPLHSKQH RTRALTPASD LHFGDAEVER CWQQANRVID  
===== ===== ===== ===== ===== =====  
301 KDIRLLILGQ TGVGKNEFKV ALHKNSQRKN GPLVAVNCGA LAKELVAAEL  
===== ===== ===== ===== ===== =====  
351 FGYYVAGAFTG ASHKGYQGKV RLADKGILFL DEIADLPLDA QSRLLHVLDQ  
===== ===== ===== ===== ===== =====  
401 KTVLPVGSNH ATKVDIQIIA ATHKNLEQLV TQGLFRQDLY YRLSDLVVEL  
===== ===== ===== ===== ===== =====  
451 PSFQQRQDRQ ALIHHIHRRY SDAGQQICGD LMQRLLAYHW PGNLRELDL  
===== ===== ===== ===== ===== =====  
501 IKVASLMAEG EGVLTFNHL P THLAQKLSHA APTATEDDQQ KDIKSTVEAS  
===== ===== ===== ===== ===== =====  
551 LLKTYQATQG NISQTSRLLG LSRNTIYRKL KALGILK  
===== ===== ===== ===== ===== =====

HITS AT: 1-587  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER  
DT.CA CAplus document type: Journal  
RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)  
      1 REFERENCES IN FILE CA (1907 TO DATE)  
      1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 42 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 290402-60-7 REGISTRY  
CN Protein (*Vibrio cholerae* strain N16961 gene VC1555) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN GenBank AAF94709  
CN GenBank AAF94709 (Translated from: GenBank AE004233)  
FS PROTEIN SEQUENCE  
SQL 170

SEQ        1 MWRLRASSIN KETPMFIGHI TQRQFCAALS PQLQRLINEV LQRVAAPLPT  
===== ===== ===== ===== ===== =====  
      51 GKHELQGDSA FFLVMEDHTQ PLALRRSECH ARYLDVQILL QGRERFGYSL  
===== ===== ===== ===== ===== =====  
  101 APFSGLDEDL LATRDVAFSA QLVEERFVDL AAGDFIVFYP GQPHRPLIAV  
===== ===== ===== ===== ===== =====

151 EGECEPVRKV VIKVDKAFFE  
=====

HITS AT: 1-170  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER  
DT.CA CAplus document type: Journal  
RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 43 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 290401-24-0 REGISTRY  
CN Protein (Vibrio cholerae strain N16961 gene VC1380) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN GenBank AAF94538  
CN GenBank AAF94538 (Translated from: GenBank AE004217)  
FS PROTEIN SEQUENCE  
SQL 116

SEQ 1 MKASELKTIQ NQLPDLDLDPD VVMGEVWLPE RLIEAQQLDDD MLFLTFDNAP  
=====  
51 EEEGEGEEGR GFVEHEMELI RSQLMTILAE DSGPKTKAEA LLALITLAHE  
=====  
101 RTSSEFIEIL GTMLEE  
=====

HITS AT: 1-116  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER  
DT.CA CAplus document type: Journal  
RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 44 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
RN 290398-85-5 REGISTRY  
CN Heat shock protein HtpX (Vibrio cholerae strain N16961 gene VC1117) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN GenBank AAF94276  
CN GenBank AAF94276 (Translated from: GenBank AE004192)  
FS PROTEIN SEQUENCE  
SQL 287

SEQ 1 MKRILLFLAT NLAVVLVLSV VLNVYAVTG MQPGSLSGLL VMAAVFGFGG  
=====  
51 AFISLLMSKS MALRSVGGVV IDTPRNEMEH WLLETVRQRQA NQAGIGMPTV  
=====  
101 AIYDAPDMNA FATGAKRDDS LVAVSTGLLH NMTRDEAEAV LAHEVSHIAN  
=====  
151 GDMVTMTLMQ GVVNTFVIFL SRFIANIVAS RDSEESEGGSN MMVYFGVSMV  
=====  
201 LELVFGFLAS FITMWYSRHR EFHADAGAAQ LVGKHKMIAA LERLKGQES  
=====  
251 HLEGSMMAFG ITGKRSLSEL MMTHPPLEKR IAALRN  
=====

HITS AT: 1-287

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 45 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290395-16-3 REGISTRY

CN Isoleucyl-tRNA synthetase (Vibrio cholerae strain N16961 gene VC0682)  
(9CI) (CA INDEX NAME)

## OTHER NAMES:

CN GenBank AAF93847

CN GenBank AAF93847 (Translated from: GenBank AE004154)

FS PROTEIN SEQUENCE

SQL 949

```

SEQ      1 MSEYKDTLNL PETGFPMRGD LAKREPEMLQ RWYQEDLYGA IRQAKKGKKS
        ===== ===== ===== ===== ===== ===== ===== ===== =====
      51 FVLHDGPPYA NGDIHIGHAL NKILKDVIK SKTLSGFADP YIPGWDCHGL
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     101 PIELMVEKKV GKPGQKVTAAC EFREKCREYA AGQVEGQKES FKRLGILGEW
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     151 DKPYRTMDFV TEANIIRALG KIADNGHLLK GFKPVHWCTD CGSALAEAEV
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     201 EYKNKVSPSI DVRFKAADEA AVLAKFGLAA GHEGKGDVSI VIWTTPWTL
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     251 PANRAVCLRA DLEYVLIQVE GEQPERIIIVA SELAKSVMDR AGIEHFHN LG
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     301 FATGADLELV QFQHPFYSFT VPAILGDHVT TDSGTGVVHT APGHGQEDFA
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     351 VGQQYQGLEVA NPVGNSGVYL PDTELFAGQH VFKANDSVLE VLKEKGALLH
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     401 HHAYEHSYPH CWRHKTPPIIF RATPQWFVSM EQAGLREQAL TAIKGVHWMP
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     451 DWGQSRIEGM VAGRPEWCIS QRRTWGVPIA LFVHKETAEL HPNSADLIEK
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     501 VAQLVEQKGI QAWWDLDTAE LLGAEDAANY EKVLDLTDVV FDSGVTHSAV
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     551 VDARQEFGNGA EADMYLEGSD QHRGWFQSSL ISSVAMKGKA PYKEVLTHGF
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     601 VVDGQGRKMS KSIGNVVAPQ DVTNKLGADI LRLWVASTDY TGEVAVSDEI
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     651 LKRSADAYRR IRNTARFFLA NLNGFNPTTD IIPVEDMVAL DRWAVGRALA
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     701 AQQEIIQAYQ DYNLHAVVQR LMNFCSIEMG SFYLDVIKDR QYTAKRGGHA
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     751 QRSCQTALFF IVEALVRWMA PIMSFTADEI WNAMPAQQAD GSARDKFVFT
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     801 TEWFDFGLFGL AEGEELNNAF WNDIQKVRGS VNKLLENARN EKLIGGSLQA
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     851 ELVLFADDSSL ASKLAKLGDE LRFVLLTSKA VVKPLAEKSE AAQATDIDGL
        ===== ===== ===== ===== ===== ===== ===== ===== =====
     901 FVQVNKTAEAE KCDRCWHHTP DVGTIAGHTT ICGRCVSNVE GEGEVRKFA
        ===== ===== ===== ===== ===== ===== ===== ===== =====

```

HITS AT: 1-949

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Cplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 46 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290392-99-3 REGISTRY

CN Dehydrogenase, malate (Vibrio cholerae strain N16961 gene VC0432) (9CI)  
(CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF93605

CN GenBank AAF93605 (Translated from: GenBank AE004130)

CN Malate dehydrogenase (Vibrio cholerae strain N16961 gene VC0432)

FS PROTEIN SEQUENCE

SQL 353

SEQ 1 MRKVAKLTLL DCNQIVITIA FDGRIHLITL QTYKRLLSRR FTMKVAVIGA

===== ===== ===== ===== ===== =====

51 AGGIGQALAL LLKNRLPAGS DLALYDIAPV TPGVAAADLSH IPTPVTIKGY

===== ===== ===== ===== ===== =====

101 AGEDPTPALE GADVVLVSAG VARKPGMDRA DLFNVNAGIV KALAEKIAVV

===== ===== ===== ===== ===== =====

151 CPKACVGIIT NPVNNTVPIA AEVLKKAGVY DKRKLFGVTT LDVIRSETFV

===== ===== ===== ===== ===== =====

201 AALKDKDPGQ VRVPVIGGHS GTVILPLLSQ VEGVSFTDEE VAAALKRIQN

===== ===== ===== ===== ===== =====

251 AGTEEVVEAKA GGGSATLSMG QAACRFLGL VKALQGESDV VEYAYVEGEG

===== ===== ===== ===== ===== =====

301 EYAPFFAQPI KLGKNGVEAL LDIGKLSAYE QAALDGMLDT LKGDIQIGVE

===== ===== ===== ===== ===== =====

351 FVK

====

HITS AT: 1-353

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Cplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 47 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 272763-00-5 REGISTRY

CN Protein JSAP1d (JNK/SAPK-associated protein-1d) (mouse) (9CI) (CA INDEX  
NAME)

OTHER NAMES:

CN 13: PN: WO0031132 SEQID: 12 claimed protein

CN JNK/SAPK-associated protein 1d (mouse gene jsap1)

CN JSAP1d protein (mouse)

CN Protein JSAP1 (JNK/stress-activated protein kinase-associated protein 1)  
(mouse gene jsap1 isoform JSAP1d)

FS PROTEIN SEQUENCE

SQL 1336

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	WO2000031132
	claimed
	SEQID 12

SEQ	Sequence
1	MMEIQMDEGG GVVVYQDDYC SG SVM SERVS GLAGSIYREF ERLIHCYDEE
51	VVKELMPLVV NVLENLDSVL SENQEHEVEL ELLREDNEQL LTQYEREKAL
101	RKQAEKKFIE FEDALEQEKK ELQIQVEHYE FQTROLELKA KNYADQISRL
151	EERESEM KKE YNALHQRHTE MIQTYVEHIE RSKMQQVGGS GQTESSLPG
201	RKERPTSLNV FPLADGMVRA QMGGKLVPAG DHWHLSDLGQ LQSSSSYQCP
251	NDEMSESGQS SAAATPSTTG TKSNTPTSSV PSAAVTPLNE SLQPLG DYVS
301	VTKNNKQARE KRNSRNMEVQ VTQEMRNVSI GMGSSDEWSD VQDIIDSTPE
351	LDVC PETRLE RTGSSPTQGI VNKA FGINTD SLYHELSTAG SEVIGDVDEG
401	ADLLGEFSVR DDFFGMGKEV GNLLLENSQL LETKNALNVV KNDLIAKVDQ
451	LSGEQEVLKKG ELEAAKQAKV KLENRIKELE EELKRVKSEA VTARREPREE
501	VEDVSSYLC ELDKIPMAQR RRFTRVEMAR VLMERNQYKE RLMELQEA VR
551	WTEMIRASRE HPSVQEKKKS TIWQFFSRLF SSSSSPPPAK RSYP SVNIHY
601	KSPTAAGFSQ RRSHALCQIS AGSRPLEFFP DDDCTSSARR EQKREQYRQV
651	REHVRNDDGR LQACGWSLPA KYKQLSPNGG QEDTRMKNVP VPVYCRPLVE
701	KDPSTKLWCA AGVNLSGWKP HEEDSSNGPK PVPGRDPLTC DREGE GEPEPKS
751	THPSPEKKKA KETPEADATS SRVWILTSTL TTSKVVIIDA NQPGTIVDQF
801	TVCNAHVLCI SSIPAASDSD YPPGEMFLDS DVNPEDSGAD GVLAGITLVG
851	CATRCNVPRS NCSSRGDT PV LDKGQGDVAT TANGKVNPSQ STEEATEATE
901	VPPDPGPSESE ATTVRPGPLT EHVF TDPAPT PSSSTQPA SE NGSESNGTIV
951	QPQVEPSGEL STTTSSAAPT MWLGAQNGWL YVHS AVANWK KCLHSIKLKD
1001	SVLSLVHVKG RVLVALADGT LAIFHRGEDG QWDLSNYHLM DLGHPHHSIR
1051	CMAVNVDRWV CGYKNK VHV VI QPKTMQIEKS FDAHPRRESQ VRQLAWIGDG
1101	VWVSIRLDST LRLYHAHTHQ HLQDVDIEPY VSKMLGTGKL GFSFVRITAL
1151	LIAGNRLWVG TGNGVVISIP LTETVVLH RG QLLGLRANKT SPTSGEGTRP
1201	GGIIHVYGDD SSDKAASSFI PYCSMAQAOQL CFHGH RDAVK FFVSVPGNVL
1251	ATLNGSVLDS PSEGPGPAAP AADAEGQKLK NALVLSGGEG YIDFRIGDGE

1301 DDETEECAGD VNQTKPSLSK AERSHIIWQ VSYTPE  
=====

HITS AT: 1-1336

## \*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA CPlus document type: Journal; Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
OCCU (Occurrence); PRP (Properties); USES (Uses)RL.NP Roles from non-patents: BIOL (Biological study); PROC (Process); PRP  
(Properties)2 REFERENCES IN FILE CA (1907 TO DATE)  
2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 48 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 272762-99-9 REGISTRY

CN Protein JSAP1c (JNK/SAPK-associated protein-1c) (mouse) (9CI) (CA INDEX  
NAME)

## OTHER NAMES:

CN 12: PN: WO0031132 SEQID: 11 claimed protein

CN JNK/SAPK-associated protein 1c (mouse gene jsap1)

CN JSAP1c protein (mouse)

CN Protein JSAP1 (JNK/stress-activated protein kinase-associated protein 1)  
(mouse gene jsap1 isoform JSAP1c)

FS PROTEIN SEQUENCE

SQL 1337

## PATENT ANNOTATIONS (PNTE):

Sequence | Patent

Source | Reference

=====

Not Given | WO2000031132

| claimed

| SEQID 11

SEQ	1 MMEIQMDEGG GVVVYQDDYC SG SVM SERVS GLAGSIYREF ERLIHCYDEE =====
	51 VVKELMPLVV NVLENLDSVL SENQEHEVEL ELLREDNEQL LTQYEREKAL =====
	101 RKQAEEKFIE FEDALEQEKK ELQIQVEHYE FQTRQLELKA KNYADQISRL =====
	151 EERESEM KKE YNALHQRHTE MIQTYVEHIE RSKMQQVGGS GQTTESSLPG =====
	201 SRKERPTSLN VFPLADGMVR AQMGGKLVP A GDHWHLSDLG QLQSSSSYQC =====
	251 P NDEMSESGQ SSAAATPSTT GTKSNTPTSS VPSAAVTPLN ESLQPLGDYV =====
	301 SVTKNNKQAR EKRNSRNMEV QVTQEMRNVS IGMGSSDEWS DVQDIIDSTP =====
	351 ELDVCPETRL ERTGSSPTQG IVNKA FGINT D SLYHELSTA GSEVIGDVDE =====
	401 GADLLGEFSV RDDFFGMGKE VGNLLLENSQ LLETKNALNV VKNDLIAKVD =====
	451 QLSGEQEVLK GELEAAKQAK VKLENRIKEL EEEKLKRVKSE AVTARREP =====
	501 EVEDVSSYLC TELDKIPMAQ RRRFTRVEMA RVLMERNQYK ERLMELQEAV =====

```

=====
551 RWTEMIRASR EHPSVQEKKK STIWQFFSRL FSSSSSPPPA KRSYPSVNIH
=====
601 YKSPTAACGS QRRSHALCQI SAGSRPLEFF PDDDCTSSAR REQKREQYRQ
=====
651 VREHVRNDDG RLQACGWSLP AKYKQLSPNG GQEDTRMKNV PVPVYCRPLV
=====
701 EKDPSKLWC AAGVNLSGWK PHEEDSSNGP KPVPGRDPLT CDREGEPEK
=====
751 STHPSPEKKK AKETPEADAT SSRWVILTST LTTSKVVIID ANQPGTIVDQ
=====
801 FTVCNAHVLC ISSIPAASDS DYPPGEMFLD SDVNPEDSGA DGVLAGITLV
=====
851 GCATRCNVPR SNCSRGDTP VLDKGQGDVA TTANGKVNP S QSTEEATEAT
=====
901 EVPDPGPSES EATTVRPGPL TEHVFTDPAP TPSSSTQPAS ENGSESNGTI
=====
951 VQPQVEPSGE LSTTTSSAAP TMWLGAQNGW LYVHSAVANW KKCLHSIKLK
=====
1001 DSVLSLVHVK GRVLVALADG TLAIFHRGED GQWDLSNYHL MDLGHPHHSI
=====
1051 RCMAVVNDRV WCGYKNKVHV IQPKTMQIEK SFDAHPRRES QVRQLAWIGD
=====
1101 GVWVSIRLDS TLRLYHAHTH QHLQDV DIEP YVSKMLGTGK LGFSFVRITA
=====
1151 LLIAGNRLWV GTGNGVVISI PLTETVVLHR GQLLGLRANK TSPTSGEGTR
=====
1201 PGGIIHVYGD DSSDKAASSF IPYCSMAQAO LCFHGHRDAV KFFVSVPGNV
=====
1251 LATLNGSVLD SPSEGPGPAA PAADAEGQKL KNALVLSGGE GYIDFRIGDG
=====
1301 EDDETEECAG DVNQTKPSLS KAERSHIIIVW QVSYTPE
=====
```

HITS AT: 1-1337

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA CAplus document type: Journal; Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); PRP (Properties); USES (Uses)

RL.NP Roles from non-patents: BIOL (Biological study); PROC (Process); PRP (Properties)

2 REFERENCES IN FILE CA (1907 TO DATE)

2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 49 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 272762-98-8 REGISTRY

CN Protein JSAP1b (JNK/SAPK-associated protein-1b) (mouse) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 11: PN: WO0031132 SEQID: 10 claimed protein

CN JNK/SAPK-associated protein 1b (mouse gene jsap1)

CN JSAP1b protein (mouse)

CN Protein JSAP1 (JNK/stress-activated protein kinase-associated protein 1) (mouse gene jsap1 isoform JSAP1b)

FS PROTEIN SEQUENCE

SQL 1314

## PATENT ANNOTATIONS (PNTE):

Sequence | Patent

Source | Reference

=====+=====

Not Given|WO2000031132

|claimed

|SEQID 10

SEQ	1 MMEIQMDEGG GVVVYQDDYC SG SVM SERVS GLAGSIYREF ERLIHCYDEE ===== ===== ===== ===== ===== =====
	51 VVKELMPLVV NVLENLDSVL SENQEHEVEL ELLREDNEQL LTQYEREKAL ===== ===== ===== ===== ===== =====
	101 RKQAEEKFIE FEDALEQEKK ELQIQVEHYE FQTRQLELKA KNYADQISRL ===== ===== ===== ===== ===== =====
	151 EERESEMKE YNALHQRHTE MIQTYVEHIE RSKMQQVGGS GQTESSLPGR ===== ===== ===== ===== ===== =====
	201 SPRQSWRKSR KERPTSLNVF PLADGMCPND EMSESGQSSA AATPSTTGTK ===== ===== ===== ===== ===== =====
	251 SNPTSSVPS AAVTPLNESL QPLGDYVSVT KNNKQAREKR NSRNMEVQT ===== ===== ===== ===== ===== =====
	301 QEMRNVSIGM GSSDEWSDVQ DIIDSTPELD VCPETRLERT GSSPTQGIVN ===== ===== ===== ===== ===== =====
	351 KAFGINTDSSL YHELSTAGSE VIGDVDEGAD LLGEFSVRDD FFGMGKEVGN ===== ===== ===== ===== ===== =====
	401 LLENSQLLE TKNALNVVKN DLIAKVDQLS GEQEVLKGEL EAAKQAKVKL ===== ===== ===== ===== ===== =====
	451 ENRIKELEEE LKRVKSEAVT ARREPREEVE DVSSYLCTEL DKIPMAQRRR ===== ===== ===== ===== ===== =====
	501 FTRVEMARVL MERNQYKERL MELQEAVRWT EMIRASREHP SVQEKKKSTI ===== ===== ===== ===== ===== =====
	551 WQFFSRLFSS SSSPPPAKRS YPSVNIHYKS PTAAGFSQRR SHALCQISAG ===== ===== ===== ===== ===== =====
	601 SRPLEFFPDD DCTSSARREQ KREQYRQVRE HVRNDDGRLQ ACGWSLPAKY ===== ===== ===== ===== ===== =====
	651 KQLSPNGGQE DTRMKNPVPV VYCRPLVEKD PSTKLWCAAG VNLSGWKPHE ===== ===== ===== ===== ===== =====
	701 EDSSNGPKPV PGRDPLTCDR EGEGEPKSTH PSPEKKKAKE TPEADATSSR ===== ===== ===== ===== ===== =====
	751 VWILTSTLTQ SKVVIIDANQ PGTIVDQFTV CNAHVLCISS IPAASDSDYP ===== ===== ===== ===== ===== =====
	801 PGEMFLDSDV NPEDSGADGV LAGITLVGCA TRCNVPRSNC SSRGDTPVLD ===== ===== ===== ===== ===== =====
	851 KGQGDVATT A NGKVNPQSQT EEATEATEVP DPGPSESEAT TVRPGPLTEH ===== ===== ===== ===== ===== =====
	901 VFTDPAPTPS SSTQPASENG SESNGTIVQP QVEPSGELST TTSSAAPTMW ===== ===== ===== ===== ===== =====
	951 LGAQNGWLYY HSAVANWKKC LHSIKLKDSV LSLVHVKGKV LVALADGTLA ===== ===== ===== ===== ===== =====
	1001 IFHRGEDGQW DLSNYHLMGL GHPHHSIRCM AVVNDRVWCY YKNKVKHVIQP ===== ===== ===== ===== ===== =====
	1051 KTMQIEKSFD AHPRRESQVR QLAWIGDGW VSIRLDSTLR LYHAHTHQHL ===== ===== ===== ===== ===== =====
	1101 QDVDIEPYVS KMLGTGKLGF SFVRITALLI AGNRLWVGTV NGVVISIPLT ===== ===== ===== ===== ===== =====
	1151 ETVVLHRGQL LGLRANKTSP TSGEGRPGG IIHVYGDSS DKAASSFIPY ===== ===== ===== ===== ===== =====
	1201 CSMAQAQLCF HGHRAVKFF VSVPGNVLAT LNGSVDSPS EGPGPAAPAA ===== ===== ===== ===== ===== =====

Rooke 10/015, 956

1251 DAEGQKLKNA LVLSGGEGYI DFRIGDGEDD ETEECAGDVN QTKPSLSKAE  
===== ===== ===== ===== =====  
1301 RSHIIVWQVS YTPE  
===== ==

HITS AT: 1-1314

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA CPlus document type: Journal; Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); PRP (Properties); USES (Uses)

RL.NP Roles from non-patents: BIOL (Biological study); PROC (Process); PRP (Properties)

2 REFERENCES IN FILE CA (1907 TO DATE)

2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 50 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 258492-41-0 REGISTRY

CN Enzyme (simian immunodeficiency virus strain SIVcpz gene pol precursor) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF18575

CN GenBank AAF18575 (Translated from: GenBank AF115393)

CN Pol polyprotein (simian immunodeficiency virus strain SIVcpz gene pol)

FS PROTEIN SEQUENCE

SQL 1013

NTE

type	-----	location	-----	description
uncommon	Aaa-471	-	-	
uncommon	Aaa-489	-	-	
uncommon	Aaa-575	-	-	

SEQ 1 FFRERLVSVE RGIKETREL P AGQEGTHSSA PRELWVSGSN RKETGGGE  
===== ===== ===== ===== =====  
51 GKGTGPVSSVN LPQITLWQRP LLGVKIEGQL IEALLDTGAD DTVIDNVQLT  
===== ===== ===== ===== =====  
101 GKWRPKMIGG IGGFIKVQY DNIAIEIEGR KTTGTVLVGP TPVNIIGRNI  
===== ===== ===== ===== =====  
151 LTQIGCTLNF PISPIETVPV KLKPGMDGPR VKQWPLTAEK IKALTEICQE  
===== ===== ===== ===== =====  
201 MEKEKGKISRI GPENPYNTPI FAIKKKDSTK WRKLVDREL NKRTQDFWEV  
===== ===== ===== ===== =====  
251 QLGIPHPAGL KKKKSVTVLD VGDAYFSCPL DENFRKYTAF TIPSVNNETP  
===== ===== ===== ===== =====  
301 GIRYQYNVLP QGWKGSPAIF QSSMIKILTP FRQQHPDLII YQYMDDLYVG  
===== ===== ===== ===== =====  
351 SDLELRHRE KVELLRQHLL TWGFTTPDKK HQKEPPFLWM GYELHPDKWT  
===== ===== ===== ===== =====  
401 VQPIQLPQKE TWTVNNDIQKL VGKLNWASQI YPGIKVKQLC KLIKGTKALT  
===== ===== ===== ===== =====  
451 DIVTMTQEAE MELEENREIL XDPVHGYYD PEKELIAEXQ KQGNSQWTYQ  
===== ===== ===== ===== =====  
501 IFQEQQHKNLK TGKYARQRSA HTNDIRQLAE VVQKIATESI VIWGKTPKFR  
===== ===== ===== ===== =====

551 LPVQKEVWET WWSEYWQATW IPDWXFVNTP PLVKLWYQLE TEPIPGAETF  
 =====  
 601 YVDGAANRET KKGKAGYVTD RGRQKIVNLE NTTNQKAELT AVYLALQDAE  
 =====  
 651 HIVNIVTDSQ YVLGIHSQP DQSESELVNL IIEELIKKEK SYLSWVPAHK  
 =====  
 701 GVGGNEQVDK LVSSGNQKSS LFRWYRLSTR KNMRKYHNNW RAMASDFNIP  
 =====  
 751 HIVAKELVAR CDKCQLKGEA MHGQVDCSPG IWQLDCTHLE GKVLILAVHV  
 =====  
 801 ASGYLEAEVI PAETGQETAY FILKLAGRWP VKVIHTDNGP NFTSNTVKAA  
 =====  
 851 CWWAGIQQEF GIPYNPQSQG VVESMNKELK KIIGQIREQA EHLRTAVQMA  
 =====  
 901 VFIFHNFKRKG GIGGYTAGER IIDIIATDIQ TTNLQKQILK VQNFRVYYRD  
 =====  
 951 SRDPIWKGP A RLLWKGEHAV VIKEREEVKV IPRRKAKIIR DYGKQMAGDD  
 =====  
 1001 SMAGGQDESQ GLE  
 =====

HITS AT: 1-1013

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 51 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 256915-31-8 REGISTRY

CN Double-stranded RNA-binding protein (human clone NT1 gene STAU2) (9CI)  
 (CA INDEX NAME)

OTHER NAMES:

CN 1899: PN: WO0153312 SEQID: 2273 claimed sequence

CN Protein (human clone 784CIF2B\_161 precursor)

FS PROTEIN SEQUENCE

SQL 479

PATENT ANNOTATIONS (PNTE):

Sequence | Patent

Source | Reference

=====+=====

Not Given | WO2001053312

| claimed

| SEQID 2273

SEQ 1 MLQINQMFSV QLSLGEQTWE SEGSSIKKAQ QAVANKALTE STLPKPVQKP  
 =====  
 51 PKSNVNNNPG SITPTVELNG LAMKRGEPAI YRPLDPKPFP NYRANYNFRG  
 =====  
 101 MYNQRYHCPV PKIFYVQLTV GNNEFFGEGK TRQAARHNAA MKALQALQNE  
 =====  
 151 PIPERSPQNG ESGKDMDDDK DANKSEISLV FEIALKRNMP VSFEVIKESG  
 =====  
 201 PPHMKSFVTR VSVGEFSAEG EGNSKKLSKK RAATTVLQEL KKLPPPLPVVE  
 =====  
 251 KPKLFFKKRP KTIVKAGPEY GQGMNPISRL AQIQQAKKEK EPDYVLLSER

```

=====
301 GMPRRREFVM QVKVGNEVAT GTGPNKKIAK KNAAEAMLLQ LGYKASTNLQ
=====
351 DQLEKTGENK GWSGPKPGFP EPTNNTPKG I LHLSPDVYQE MEASRHKVIS
=====
401 GTTLGYLSPK DMNQPSSFF SISPTSNSSA TIARELLMNG TSSTAEEAIGL
=====
451 KGSSPTPPCS PVQPSKQLEY LARIQGFQV
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HITS AT: 1-479

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA CAplus document type: Journal; Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);  
OCCU (Occurrence); PRP (Properties); USES (Uses)

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

2 REFERENCES IN FILE CA (1907 TO DATE)

2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 52 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 247916-06-9 REGISTRY

CN Protein mAKAP (muscle A-kinase anchoring protein) (Rattus norvegicus  
strain Sprague-Dawley) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAD39150

CN GenBank AAD39150 (Translated from: GenBank AF139518)

CN Protein mAKAP (muscle A-kinase anchoring protein) (rat strain  
Sprague-Dawley)

FS PROTEIN SEQUENCE

SQL 2314

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SEQ      1 MLTMSVTLSP LRSQGPDPMA TDASPMAINM TPTVEQEEGE GEEAVKAIDA
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51 EQQYGKPPPL HTAADWKIVL HLPEIETWLR MTSEVRDLT YSVQQDADSK
=====
101 HVDVHLVQLK DICEDISDHV EQIHALLETE FSLKLLSYSV NVIVDIHAVQ
=====
151 LLWHQLRVSV LVLRERILQG LQDANGNYTR QTDILQAFSE ETTEGRLDLS
=====
201 TEVDDSGQLT IKCSQDYLSL DCGITAFELS DYSPSEDLLG GLGDMTTSQA
=====
251 KTKSFDSWSY SEMEKEFPEL IRSVGLLTVA TEPVPSSCGE ANEDSSQASL
=====
301 SDDHKGEHGE DGAPVPGQQL DSTVGMSLSD GTLANAAEHP SETAKQDSTS
=====
351 SPQLGAKKTQ PGPCEITTPK RSIRDCFNYN EDSPTQPTLP KRGLFLKETQ
=====
401 KNERKGSDRK GQVVDLKPEL SRSTPSLVDP PDRSKLCLVL QSSYPSSPSA
=====
451 ASQSYECLHK VGLGNLENIV RSHIKEISSS LGRLTDCHKE KLRLKKPHKT
=====
501 LAEVSLCRIP KQGGGSGKRS ESTGSSAGPS MVSPGAPKAT MRPETDSAST
=====
551 ASGGLLCHQRN RSGQLPVQSK ASSSPPCSHS SESSLGSDSI KSPVPLL SKN
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601 KSQKSSPPAP CHATQNGQVV EAWYGSDEYL ALPSHLKQTE VLALKLES LT
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```

=====
651 KLLPQKPRGE TIQDIDDWEL SEMNSDSEIY PTYHIKKHT RLGTVSPSSS
=====
701 SDIASSLGES IESGPLSDIL SDEDLCLPLS SVKKFTDEKS ERPSSSEKNE
=====
751 SHSATRSALI QKLMHDIQHQ ENYEAIWERI EGFVNKLDEF IQWLNEAMET
=====
801 TENWTPPKAE TDSLRLYLET HLSFKLNVDS HCALKEAVEE EGHQLLELVV
=====
851 SHKAGLKDTL RMIASQWKEL QRQIKRQHSW ILRALDTIKA EILATDVSVE
=====
901 DEEGTGSPKA EVQLCHLETQ RDAVEQMSLK LYSEQYTSGS KRKEEFANMS
=====
951 KAHAEGSNGL LDFDSEYQEL WDWLIDMESL VMDSHDLMMS EEQQQHLYKR
=====
1001 YSVEMSIHL KKSELLSKVE ALKKGGSLSP DDILEKVDSI NEKWELLGKT
=====
1051 LREKIQDTIA GHSGSGPRDL LSPESGSLVR QLEVRIKELK RWLRDTELF
=====
1101 FNSCLRQEKE GTSAEKQLQY FKSLCREIKQ RRRGVASILR LCQHLLDDRD
=====
1151 TCNLNADHQP MQLIIVNLER RWEAIVMQAV QWQTRLQKKM GKESETLNU
=====
1201 DPGLMDLNGM SEDALEWDET DISNKLISVH EESNDLDQDP EPMLPAVKLE
=====
1251 ETHHKDGSYE EEAGDCGGSP YTTSNITAPSS PHIYQVYSLH NVELHEDSHT
=====
1301 PFLKSSPKFT GTTQPTVLTK SLSKDSSFSS TKSLPDLLGG SGLVRPYSCH
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1351 SGDLSQNSGS ESGIVSEGDN EMPTNSDMSL FSMVDGSPSN PETEHPDPM
=====
1401 GDAANVLEQK FKDNGESIKL SSVSRASVSP VGCVNGKAGD LNSVTKHTAD
=====
1451 CLGEELQGKH DVFTFYDYSY LQGSKLKLPIM MKQPQSEKA HVEDPLLGGF
=====
1501 YFDKKSCAK HQASESQPDA PPHERILASA PHEMGRSAYK SSDIEKTFTG
=====
1551 IQSARQLSSL SRSSSVESLS PGGDLFGLGI FKNGSDSLQR STSLESWLTS
=====
1601 YKSNEDELFC HSSGDISVSS GSVGELSKRT LDLLNRLENI QSPSEQKIKR
=====
1651 SVSDMTLQSS SQKMPFAGQM SLDVASSINE DSPASLTLS SSDELSLCSE
=====
1701 DIVLHKKNIP ESNASFRKRL NRVADESVD NVSMIVNVSC TSACTDDEDD
=====
1751 SDLLSSSTLT LTEEELCLKD EDDDSIATD DEIYEESNLM SGLDYIKNEL
=====
1801 QTWIRPKLSL TREKKRSGVT DEIKVNKG D GNEKANPSDT LDIEALLNGS
=====
1851 IRCLSENNNG GTKPPRTHGS GTKGENKKST YDVSKDPHVA DMENGNIEST
=====
1901 PEREREKPGQ LPEVSENLAS NVKTISESEL SEYEAVMDGS EDSSVARKEF
=====
1951 CPPNDRHPPQ MGPKLQHPEN QSGDCKPVQN PCPGLLSEAG VGSRQDSNGL
=====
2001 KSLPNDAPOSG ARKPAGCCLL EQNETEESAS ISSNASCCNC KPDVFHQKDD
=====
2051 EDCSVHDFVK EIIDMASTAL KSKSQPESEV AAPTSLTQIK EKVLEHSHRP
=====
2101 IHLRKGDFYS YLSLSSHDS CGEVTNYIDE KSSTPLPPDA VDSGLDDKED

```

===== ===== ===== ===== =====  
2151 MDCFFEACVE DEPVNEEAGL PGALPNESAI EDGAEQKSEQ KTASSPVLS  
===== ===== ===== ===== =====  
2201 KTDLVPLSGL SPQKGADDAK EGDDVSHTSQ GCAESTEPTT PSGKANAEGR  
===== ===== ===== ===== =====  
2251 SRMQGVSATP EENAASAKPK IQAFSLNAKQ PKGKVAMRYP SPQTLTCKEK  
===== ===== ===== ===== =====  
2301 LVNFHEDRHS NMHR  
===== =====

HITS AT: 1-2314

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA CPlus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); OCCU (Occurrence);  
PROC (Process); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 53 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 211809-45-9 REGISTRY

CN Docking protein DP (human gene HsPex14p peroxisome-associated) (9CI) (CA  
INDEX NAME)

OTHER NAMES:

CN Peroxin (Cricetulus longicaudatus CHO-K1 gene Pex14)

CN Peroxisomal membrane anchor protein (Cricetulus longicaudatus CHO-K1 gene  
Pex14)

FS PROTEIN SEQUENCE

SQL 377

SEQ 1 MASSEQAEQP SQPSSTPGSE NVLPREPLIA TAVKFLQNSR VRQSPLATRR  
===== ===== ===== ===== =====  
51 AFLKKKG LTD EEIDMAFQQS GTAADEPSSL GPATQVVPVQ PPHLISQPYS  
===== ===== ===== ===== =====  
101 PAGSRWRDYG ALAIIMAGIA FGFHQLYKKY LLPLILGGRE DRKQLERMEA  
===== ===== ===== ===== =====  
151 GLSELSGSVA QTVTQLQTTL ASVQELLIQQ QQKIQELAHE LAAAKATTST  
===== ===== ===== ===== =====  
201 NWILESQNIN ELKSEINSLK GLLLNRRQFP PSPSAPKIPS WQIPVKSPSP  
===== ===== ===== ===== =====  
251 SSPAAVNHHSS SSDISPVSNE STSSSPGKEG HSPEGSTVTVY HLLGPQEEGE  
===== ===== ===== ===== =====  
301 GVVDVKGQVR MEVQGEEEKR EDKEDEEDEE DDDVSHVDEE DCLGVQREDR  
===== ===== ===== ===== =====  
351 RGGDGQINEQ VEKLRRPEGA SNESERD  
===== ===== ===== =====

HITS AT: 1-377

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CPlus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

2 REFERENCES IN FILE CA (1907 TO DATE)

2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 54 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 209277-31-6 REGISTRY  
 CN Kinase (phosphorylating), gene flrB protein (Vibrio cholerae strain 0395)  
     (9CI) (CA INDEX NAME)  
 OTHER NAMES:  
 CN Sensory box sensor histidine kinase (Vibrio cholerae strain N16961 gene  
     VC2136)  
 FS PROTEIN SEQUENCE  
 SQL 351

SEQ       1 MMSSAVQEQQ SHLDSLEDQV ERYKQVLDVM PAGVILLDTQ GIVREANPEA  
       ===== ===== ===== ===== =====  
       51 QRLLDVPLVG EKWYSVIQIA FAPRDDDGE ISLRNGRKVR LAISASTTQG  
       ===== ===== ===== ===== =====  
       101 LILITDLTET RLLQSRSISDL QRLSSLGRMV ASLAHQVRTP LSSAMLYAAN  
       ===== ===== ===== ===== =====  
       151 LAAPNLPPAT RERFQSKLVD RLHDLEKQVN DMLLFAKGGD NKVVMPFSIG  
       ===== ===== ===== ===== =====  
       201 DLAAEFMPMV ETALKNNQID YQQEVESEET MLLGNANALA SALSNLVMNA  
       ===== ===== ===== ===== =====  
       251 LQIAGKGSQI DVFFRPVNGE LKISVQDNGP GVPESLQHKG MEPFFTRRSQ  
       ===== ===== ===== ===== =====  
       301 GTGLGLAVVQ MVCRAHGGRL ELISKEGEGA CFTMCIPLER QADSSNSETG  
       ===== ===== ===== ===== =====  
       351 E  
       =

HITS AT: 1-351

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
 CI MAN  
 SR CA  
 LC STN Files: CA, CAPLUS, TOXCENTER  
 DT.CA CAplus document type: Journal  
 RL.NP Roles from non-patents: BIOL (Biological study); PROC (Process); PRP  
     (Properties)  
           2 REFERENCES IN FILE CA (1907 TO DATE)  
           2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 55 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
 RN 179310-03-3 REGISTRY  
 CN Phosphatase, phosphoprotein (phosphotyrosine) (human clone hPtP $\kappa$   
     isoenzyme  $\kappa$ ) (9CI) (CA INDEX NAME)  
 OTHER NAMES:  
 CN GenBank CAA94519  
 CN GenBank CAA94519 (Translated from: GenBank Z70660)  
 FS PROTEIN SEQUENCE  
 SQL 1439

SEQ       1 MDTTAAAALP AFVALLLLSP WPLLGSQAQQ FSAGGCTFDD GPGACDYHQL  
       ===== ===== ===== ===== =====  
       51 LYDDFEWVHV SAQEPHYLPP EMPQGQSYMIV DSSDHDPGEK ARLQLPTMKE  
       ===== ===== ===== ===== =====  
       101 NDTHCIDFSY LLYSQKGLNP GTLNILVRVN KGPLANPIWN VTGFTGRDWL  
       ===== ===== ===== ===== =====  
       151 RAELEVSSFW PNEYQVIFEA EVSGGGRSGYI AIDDIQVLSY PCDKSPHFLR  
       ===== ===== ===== ===== =====  
       201 LGDVEVNAGQ NATFOCIATG RDAVHNKLWL QRNRNGEDIPV AQTKNINHRR  
       ===== ===== ===== ===== =====  
       251 FAASFRLQEV TKTDQDLYRC VTQSERGSGV SNFAQLIVRE PPRPIAPPQL  
       ===== ===== ===== ===== =====

301 LGVGPTYLLI QLNANSIIIGD GPIILKEVEY RMTSGSWTET HAVNAPTYKL  
 =====  
 351 WHLDPDTEYE IRVLLTRPGE GGTGLPGPPL ITRTKCAEPM RTPKTLKIAE  
 =====  
 401 IQARRIAVDW ESLGYNITRC HTFNVTICYH YFRGHNESKA DCLDMDPKAP  
 =====  
 451 QHVVNHLPPY TNVSLKMLT NPEGRKESEE TIIQTDEDVP GPVPVKSLQG  
 =====  
 501 TSFENKIFLN WKEPLDPNGI ITQYEISYSS IRSFDPAVPV AGPPQTVSNT  
 =====  
 551 WNSTHHVFMH LHPGTTYQFF IRASTVKGFG PATAINVTTN ISAPTLPDYE  
 =====  
 601 GVDASLNETA TTITVLLRPA QAKGAPISAY QIVVEELHPH RTKREAGAME  
 =====  
 651 CYQVPVTYQN AMSGGAPYYF AAEELPPGNLP EPAPFTVGDN RTYQGFWNPP  
 =====  
 701 LAPRKGYNIY FQAMSSVEKE TKTQCVRIAT KAATEEPEVI PDPAKQTDRV  
 =====  
 751 VKIAGISAGI LVFILLLLVV ILIVKKSKLA KKRKDAMGNT RQEMTHMVNA  
 =====  
 801 MDRSYADQST LHAEDPLSIT FMDQHNFSPR YENHSATAES SRLLDVPRYL  
 =====  
 851 CEGTESPYQT GQLHPAIRVA DLLQHINLMK TSDSYGFKEE YESFFEGQSA  
 =====  
 901 SWDVAKKDQN RAKNRYGNII AYDHRSVILQ PVEDDPSSDY INANYIDGYQ  
 =====  
 951 RPSHYIATQG PVHETVYDFW RMIWQEQSAC IVMVTNLVEV GRVKCYKYWP  
 =====  
 1001 DDTEVYGDfk VTCVEMEPLA EYVVRTFTLE RRGYNEIREV KQFHFTGWPD  
 =====  
 1051 HGVPYHATGL LSFIRRVKLS NPPSAGPIVV HCSAGAGRIG CYIVIDIMLD  
 =====  
 1101 MAEREGVVDI YNCVKALRSR RINMVQTEEQ YIFIHDAILE ACLCGETAIP  
 =====  
 1151 VCEFKAAYFD MIRIDSQTNS SHLKDEFQTL NSVTPRLQAE DCSIACLPRN  
 =====  
 1201 HDKNRFMDML PPDRCPLFLI TIDGESSNYI NAALMDSYRQ PAAFIVTQYP  
 =====  
 1251 LPNTVKDFWR LVYDYGCTSI VMLNEVDLSQ GCPQYWPEEG MLRYGPIQVE  
 =====  
 1301 CMSCSMDCDV INRIFRICNL TRPQEGYLMV QQFQYLGWAS HREVPGSKRS  
 =====  
 1351 FLKLILQVEK WQEECEEGER RTIIHCLNGG GRSGMFCAIG IVVEMVKRQN  
 =====  
 1401 VVDVFHAVKT LRNSKPNMVE APEQYRFCYD VALEYLESS  
 =====

HITS AT: 1-1439

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); OCCU (Occurrence);  
PROC (Process); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

RN 174597-29-6 REGISTRY  
 CN Protein (*Thermus aquaticus* strain YT1 gene mutS DNA mismatch repair) (9CI)  
 (CA INDEX NAME)  
 OTHER NAMES:  
 CN Phosphatase, adenosine tri- (*Thermus aquaticus* strain YT1 gene mutS)  
 FS PROTEIN SEQUENCE  
 SQL 811

SEQ        1 MEGMLKGEGP GPLPPLLQQY VELRDQYPDY LLLFQVGDFY ECFGEDAERL  
 =====  
 51 ARALGLVLTH KTSKDFTTPM AGIPLRAFEA YAERLLKMGF RLAVADQVEP  
 =====  
 101 AEEAEGLVRR EVTQLLTPGT LLQESLLPRE ANYLAAIATG DGWGLAFLDV  
 =====  
 151 STGEFKGTVL KSKSALYDEL FRHRPAEVLL APELLENGAF LDEFRKRFPV  
 =====  
 201 MLSEAPFEPE GEGPLALRRA RGALLAYAQR TQGGALSLQP FRFYDPGAFM  
 =====  
 251 RLPEATLRLA EVFEPLRGQD TLFSVLDETR TAPGRRLLQS WLRHPLLDRG  
 =====  
 301 PLEARLDRVE GFVREGALRE GVRRLLYRLA DLERLATRLE LGRASPDKLG  
 =====  
 351 ALRRSLQILP ELRALLGEEV GLPDLSPLKE ELEAALVEDP PLKVSEGLI  
 =====  
 401 REGYDPDLDA LRAAHREGVA YFLELEERER ERTGIPTLKV GYNAVFGYYL  
 =====  
 451 EVTRPYYERV PKEYRPVQTL KDRQRYTLPE MKEKEREVYR LEALIRRREE  
 =====  
 501 EVFLEVRERA KRQAEALREA ARILAELDVY AALAEVAVRY GYVRPRFGDR  
 =====  
 551 LQIRAGRHPV VERRTEFVPN DLEMAHELVL ITGPNMAGKS TFLRQTALIA  
 =====  
 601 LLAQVGSFVP AEEAHLPLFD GIYTRIGASD DLAGGKSTFM VEMEEVALIL  
 =====  
 651 KEATENSLVL LDEVGRGTSS LDGVIAITAV AEALHERRAY TLFATHYFEL  
 =====  
 701 TALGLPRLKN LHVAAREEAG GLVFYHQVLP GPASKSYGVE VAAMAGLPKE  
 =====  
 751 VVARARALLQ AMAARREGAL DAVLERLLAL DPDRLTPLEA LRLLQELKAL  
 =====  
 801 ALGAPLDTMK G  
 =====

HITS AT: 1-811

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
 CI MAN  
 SR CA  
 LC STN Files: CA, CAPLUS  
 DT.CA Cplus document type: Journal  
 RL.NP Roles from non-patents: BIOL (Biological study); OCCU (Occurrence);  
 PREP (Preparation); PROC (Process); PRP (Properties)  
 1 REFERENCES IN FILE CA (1907 TO DATE)  
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 57 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN  
 RN 161631-10-3 REGISTRY  
 CN Phosphatase, adenosine tri- (*Helicobacter pylori* clone pBHpC8 gene copA)  
 (9CI) (CA INDEX NAME)  
 OTHER CA INDEX NAMES:

CN Phosphatase, adenosine tri- (Campylobacter pyloridis clone pBHpc8 gene copA)  
 FS PROTEIN SEQUENCE  
 SQL 611

SEQ        1 MHWGRDFYIQ GFKALWHRQP NMSSLIAIGT SAALISSLWQ LYLVYTDHYT  
           ===== ===== ===== ===== ===== =====  
       51 DQWSYGHYYF ESVCVILMFV MVGKRIENVS KDKALDAMQA LMKNAPKTAL  
           ===== ===== ===== ===== ===== =====  
 101 KIQNDQQIEV LVDSIVVGDI LVKLPGLTLIA VDGEEIEGEG ELDESMLSGE  
           ===== ===== ===== ===== ===== =====  
 151 ALPVYKKVGD KVFSGTFNH TSFLMKATQN NKNSTLSQIV EMIHNAQSSK  
           ===== ===== ===== ===== ===== =====  
 201 AEISRLADKV SSVFVPSVIA IAILAFVVWL IIAPKPDFWW NFGIALEVVF  
           ===== ===== ===== ===== ===== =====  
 251 SVLVISCPSC FRIGYAMSIL VANQKSEFFR IIFKDAKSLE KARLVNTIVF  
           ===== ===== ===== ===== ===== =====  
 301 DKTGTLTNGK PVVKSVHSKI ELLELLSLAN SIEKSSEHVI AKGIVEYAKE  
           ===== ===== ===== ===== ===== =====  
 351 HNAPLKEMSE VKVKTGFGIS AKTDYQGTKE IIKVGNSEFF NPINTLEIQE  
           ===== ===== ===== ===== ===== =====  
 401 NGNFSLVGRA INEKEDELLG AFVLEDLPKK GVKEHVAQIK NLGINFLS  
           ===== ===== ===== ===== ===== =====  
 451 GDNRENVKKC ALELGIDGYI SNAKPQDKLN KIKELKEKGR IVMMVGDGLN  
           ===== ===== ===== ===== ===== =====  
 501 DAPSLAMSDV AVVMAKGSDV SVQAADIVSF NNNDIKSVYSA IKLSQATIKN  
           ===== ===== ===== ===== ===== =====  
 551 IKENLFWAFC YNSVFIPLAC GVLYKANIML SPAIAGLAMS LSSVSVVLNS  
           ===== ===== ===== ===== ===== =====  
 601 QRLRNFKIKD H  
           ===== =

HITS AT: 1-611

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Cplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

    1 REFERENCES IN FILE CA (1907 TO DATE)

    1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 58 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 148500-01-0 REGISTRY

CN Protein (human gene RING1 reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN Gene RING1 protein (human)

CN Protein (human clone Y42 gene RING1 ring-finger)

CN Ring finger protein 1 (human clone 1033B10 gene dJ1033B10.6)

FS PROTEIN SEQUENCE

SQL 377

SEQ        1 MDGTEIAVSP RSLHSELMCP ICCLDMNKNTM TTKECLHRFC SDCIVTALRS  
           ===== ===== ===== ===== ===== =====  
       51 GNKECPTCRK KLVSKRSLRP DPNFDALISK IYPSREEYE A HQDRVLIRLS  
           ===== ===== ===== ===== ===== =====  
 101 RLHNQQALSS SIEEGLRMQA MHRAQRVRRP IPGSDQTGTTM SGGEGEPEG  
           ===== ===== ===== ===== ===== =====  
 151 EGDGEDVSSD SAPDSAPGPA PKRPRGGGAG GSSVGTGGGG TGGVGGGAGS  
           ===== ===== ===== ===== ===== =====  
 201 EDSGDRGGT LGGTLGPPSP PGAPSPEPG GEIELVFRPH PLLVEKGEYC

Rooke 10/015, 956

===== ===== ===== ===== =====  
251 QTRYVKTTGN ATVDHLSKYL ALRIALERRQ QQEAGEPGGP GGGASDTGGP  
===== ===== ===== ===== =====  
301 DCGGEGGGGA GGGDGPEEPA LPSLEGVSEK QYTIYIAPGG GAFTTLNGSL  
===== ===== ===== ===== =====  
351 TLELVNEKFW KVSRPLELCY APTKDPK  
===== ===== =====

HITS AT: 1-377

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

3 REFERENCES IN FILE CA (1907 TO DATE)

3 REFERENCES IN FILE CAPLUS (1907 TO DATE)

Rooke 10/015,956

=> d cost

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
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SEARCH CHARGES	0.00	229.20
DISPLAY CHARGES	0.00	435.82
OTHER CHARGES	0.00	10.50
FULL ESTIMATED COST	2.45	1044.75

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-9.49

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